



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 114657

TO: Rita Mitra
Location: rem/3b65
Art Unit: 1653
Thursday, February 19, 2004

Case Serial Number: 09/786260

From: Barb O'Bryen
Location: Biotech-Chem Library
Remsen E01A69
Phone: 571-272-2518 *BOB*

barbara.obryen@uspto.gov

Search Notes

oligo search

O'Bryen, Barbara

From: Mitra, Rita
Sent: Thursday, February 19, 2004 2:43 PM
To: O'Bryen, Barbara
Subject: RE: serach ready

Barbara

Thanks a lot.

I see that in database A_Geneseq_19Jun03, there are 30 hits with 100% homology. Could you please print them all (hit no. beyond 15) for me?

Rita

-----Original Message-----

From: O'Bryen, Barbara
Sent: Thursday, February 19, 2004 10:20 AM
To: Mitra, Rita
Subject: serach ready

You can pick it up at the Information Desk in the library.

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

protein - protein search, using sw model

on: February 18, 2004, 14:39:00 ; Search time 41 Seconds
(without alignments)
460.694 Million cell updates/sec

le: US-09-786-260-1
fect score: 119
ence: 1 MKVLISLLILLPLMLSMV.....SRACQFLKQCQIRSFALPL 119

ring table: OLIGO
Gapop 60.0 , Gapext 60.0

rched: 1107863 seqs, 158726573 residues

d size : 0
al number of hits satisfying chosen parameters: 1107863

imum DB seq length: 0
imum DB seq length: 2000000000

t-processing: Listing first 45 summaries

abase : A.Geneseq.19Jun03.*
1: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
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21: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

ult No.	Score	Query Match	Length	ID	Description
1	119	100.0	119	21	Human secreted pro
2	119	100.0	119	21	Human TGC-440 secr
3	119	100.0	119	21	Human signal pepti
4	119	100.0	119	21	Membrane-bound pro
5	119	100.0	119	22	Human PRO polypept
6	119	100.0	119	22	Amino acid sequenc
7	119	100.0	119	22	Human PRO842. Hom
8	119	100.0	119	22	Human PRO842. UNQ4
9	119	100.0	119	23	Human cytokine PRO

10	119	100.0	119	23	ABG95863	Human secreted/tra
11	119	100.0	119	24	ABU71181	Human PRO842 prote
12	119	100.0	119	24	ABU71518	Human secreted pol
13	119	100.0	119	24	ABU71964	Novel human secret
14	119	100.0	119	24	ABU72121	Human PRO polypept
15	119	100.0	119	24	ABU65638	Human secreted/tra
16	119	100.0	119	24	ABU65971	Novel human secret
17	119	100.0	119	24	ABU67475	Human secreted/tra
18	119	100.0	119	24	ABU65333	Human PRO polypept
19	119	100.0	119	24	ABU59084	Novel human secret
20	119	100.0	119	24	ABU59231	Human secreted/tra
21	119	100.0	119	24	ABU59380	Novel human secret
22	119	100.0	119	24	ABU60515	Human secreted/tra
23	119	100.0	119	24	ABU58006	Human PRO polypept
24	119	100.0	119	24	ABU58469	Human PRO polypept
25	119	100.0	119	24	ABU58937	Human secreted/tra
26	119	100.0	119	24	ABU56005	Human secreted/tra
27	119	100.0	119	24	ABU57000	Human PRO polypept
28	119	100.0	119	24	ABU13897	Human PRO842 polyp
29	119	100.0	119	24	ABU10579	Human secreted/tra
30	119	100.0	119	24	ABU10852	Human PRO polypept
31	97	81.5	97	21	AA182454	Mature human TGC-4
32	93	78.2	93	19	AAW83953	Polypeptide encode
33	69	58.0	69	20	AAV11732	Human 5' EST secre
34	37	31.1	64	19	AAW83938	Human secreted pro
35	24	20.2	48	20	AAV11731	Human 5' EST secre
36	13	10.9	97	21	AAV82458	Mature mouse TGC-4
37	13	10.9	119	21	AAV82457	Mouse TGC-440 secr
38	9	7.6	144	21	AAQ09686	Arabidopsis thalia
39	8	6.7	58	22	AAU22441	Human cardiovascu
40	8	6.7	60	22	ABG57426	Human liver peptid
41	8	6.7	60	22	ABE41994	Peptide #9500 enco
42	8	6.7	60	22	ABE25625	Protein #7624 enco
43	8	6.7	60	22	AAW62872	Human brain expres
44	8	6.7	60	22	AAW75685	Human bone marrow
45	8	6.7	60	22	AAW35795	Peptide #9832 enco

ALIGNMENTS

RESULT 1
AAB34728
ID AAB34728 standard; Protein; 119 AA.

XX	AA	AAB34728;
XX	DT	26-JAN-2001 (first entry)
XX	DE	Human secreted protein encoded by DNA clone vq8 1.
XX	KW	Secreted protein; human; autoimmune disorder; multiple sclerosis; ulcer;
XX	KW	systemic lupus erythematosus; rheumatoid arthritis; anaemia; stroke;
XX	KW	haematopoiesis regulation; tissue regrowth; wound healing; haemophilia;
XX	KW	Alzheimer's disease; Parkinson's disease; Shy-drager syndrome; cancer;
XX	KW	contraceptive; infection; growth inhibition; hyperproliferative disorder;
XX	OS	psoriasis.
XX	OS	Homo sapiens.
XX	PN	WO200055375-A1.
XX	PD	21-SEP-2000.
XX	PF	17-MAR-2000; 2000WO-US07285.
XX	PR	17-MAR-1999; 99US-0124808.
XX	PR	17-MAR-1999; 99US-0124916.
XX	PR	17-AUG-1999; 99US-0149639.
XX	PR	01-OCT-1999; 99US-0157247.
XX	PR	29-NOV-1999; 99US-0167824.
XX	PR	15-FEB-2000; 2000US-0182711.

(ALPH-) ALPHAGENE INC.

Valenzuela D, Yuan O, Hoffman H, Hall J, Rapleyko P;

WPI; 2000-638211/61.

N-PSDB; AAC59829.

Novel proteins and polypeptides useful for the treatment of e.g multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, cancer, Alzheimer's disease, Parkinson's disease, stroke, anemia and ulcers -

Claim 92; Page 441-442; 493pp; English.

This invention relates to 59 human secreted proteins and the nucleotide sequences encoding them. Sequences AAC59788-C59846 and AAB34687-B34745 represent the proteins and their encoding nucleotide sequences, and sequences AAB34746-B34771 represent fragments of the proteins. Probes for the DNA sequences are represented by sequences AAC59847-C59596. The proteins exhibit neuroprotective, dermatological, immunosuppressive, antiinflammatory, antianaemic, nootropic, antiparkinsonian, cerebroprotective, haemostatic, vulnetary, cyostatic, antipsoriatic, antibacterial, virucide, and fungicide activity. The proteins and nucleotide sequences are useful as nutritional sources or supplements and in research. The proteins are useful for treating immune deficiency and disorders, which may be genetic or resulting from infections, autoimmune disorders such as multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, and for treating myeloid or lymphoid cell deficiencies such as anaemias by regulating haematopoiesis. The proteins are also useful in compositions for bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, for wound healing, tissue repair and replacement and in the treatment of wounds, incisions and ulcers. Other uses include in the treatment of central and peripheral nervous system and neuropathies such as Alzheimer's and Parkinson's diseases and Shy-Drager syndrome, and mechanical and traumatic disorders such as spinal cord disorders, head trauma and strokes. The proteins may also be used as a contraceptive, and for treating coagulation disorders such as haemophilias. The protein and nucleotide sequences with cadherin activity are useful for treating cancer. Other uses for the protein include for inhibiting the growth, infection or function of, or killing, infectious agents such as bacteria, virus, fungi and other parasites, for effecting bodily characteristics such as height, weight, hair colour, effecting biorhythms or cardiac cycles or rhythms, effecting metabolism, catabolism, anabolism, lipid processing, utilization, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, cofactors, effecting behavioural characteristics, providing analgesic effects and for treating hyperproliferative disorders such as psoriasis.

Sequence 119 AA;

Query Match 100.0%; Score 119; DB 21; Length 119;

Best Local Similarity 100.0%; Pred. No. 3.3e-110;

Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MKVLISLLLLPLMLMSVSSSLNPGVARGHRDRCQASRRWLQGGQCECKDWFRLAP 60

1 MKVLISLLLLPLMLMSVSSSLNPGVARGHRDRCQASRRWLQGGQCECKDWFRLAP 60

61 RRKFMVSLPKKQPCDHFPGKGNVKTQRHRRKPNKHSRACQFLKQCQLRSFALPL 119

61 RRKFMVSLPKKQPCDHFPGKGNVKTQRHRRKPNKHSRACQFLKQCQLRSFALPL 119

SULT 2
Y82453

AA182453 standard; Protein; 119 AA.

AA182453;

30-JUN-2000 (first entry)

Human TGC-440 secretory protein SEQ ID NO:1.

XX TGC-440; secretory protein; immunological disease; infectious disease;
KW pulmonary function disorder; hepatic function disorder; nephrotropic;
KW gastrointestinal function disorder; antiinflammatory; immunomodulatory;
KW virucide; hepatotropic; antiasthmatic; antibacterial; vaccine;
KW hepatitis; nephritis; influenza; asthma; pulmonary hypertension;
KW pneumonia; Helicobacter pylori infection.

OS Homo sapiens.

XX WO200014226-A1.

XX 16-MAR-2000.

XX

XX 02-SEP-1999; 99WO-JP04765.

XX 03-SEP-1998; 98JP-0250108.

XX (TAKE) TAKEDA CHEM IND LTD.

XX Itoh Y, Ogi K, Tanaka H, Kitada C;

XX WPI; 2000-356978/22.

XX N-PSDB; AAA08343, AAA08344.

XX Secretory protein TGC440, antibodies to it and compounds promoting or

XX inhibiting its activity for diagnosis and treatment of diseases of the

XX immune system, lung, kidney, liver and intestinal system

XX Claim 1; Fig 1; 86pp; Japanese.

XX The present sequence represents a human secretory protein designated

XX TGC-440. TGC-440 has antiinflammatory, nephrotropic, immunomodulatory,

XX virucide, hepatotropic, antiasthmatic and antibacterial activities,

XX and can be used in vaccines. TGC-440 and the polynucleotide sequence

XX encoding it can be used to treat, prevent and diagnose immunological,

XX lung, liver, kidney or gastrointestinal disorders and infectious

XX diseases, such as hepatitis, nephritis, influenza, asthma, pneumonia,

XX pulmonary hypertension, and Helicobacter pylori infection. An antibody

XX immunospecific for TGC-440 is also useful in the above treatment and

XX diagnosis, and also for quantifying the amount of TGC-440 in a liquid

XX specimen.

XX Sequence 119 AA;

Query Match 100.0%; Score 119; DB 21; Length 119;

Best Local Similarity 100.0%; Pred. No. 3.3e-110;

Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MKVLISLLLLPLMLMSVSSSLNPGVARGHRDRCQASRRWLQGGQCECKDWFRLAP 60

1 MKVLISLLLLPLMLMSVSSSLNPGVARGHRDRCQASRRWLQGGQCECKDWFRLAP 60

61 RRKFMVSLPKKQPCDHFPGKGNVKTQRHRRKPNKHSRACQFLKQCQLRSFALPL 119

61 RRKFMVSLPKKQPCDHFPGKGNVKTQRHRRKPNKHSRACQFLKQCQLRSFALPL 119

RESULT 3

AA182453

ID AA182453 standard; Protein; 119 AA.

XX AA182453;

XX 11-MAY-2000 (first entry)

XX Human signal peptide containing protein HSPP-94 SEQ ID NO:94.

XX Human; signal peptide-containing protein; HSPP; diagnosis; cancer;

XX inflammation; cardiovascular disease; anticancer; anti-inflammatory;

XX antimicrobial; nootropic; neuroprotective; cardiovascular; hepatotropic;

XX antiasthmatic; gene therapy; cell proliferation; neurological disorder;

XX reproductive disorder; developmental disorder; arteriosclerosis;

cirrhosis; psoriasis; acquired immune deficiency syndrome; anaemia;
asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia;
Parkinson's disease; Huntington's diseases; ovulatory defect;
muscular dystrophy.

Homo sapiens.

W0200000610-A2.

06-JAN-2000.

25-JUN-1999; 99WO-US14484.

26-JUN-1998; 98US-0090762.

31-JUL-1998; 98US-0094983.

01-OCT-1998; 98US-0102686.

11-DEC-1998; 98US-0112129.

(INCY-) INCYTE PHARM INC.

Lal P, Tang YT, Gorgone GA, Corley NC, Guegler KJ, Baughn MR;
Akerblom IE, Au-Young J, Yue H, Patterson C, Reddy R, Hillman JL;
Bandman O;

WPI: 2000-160673/14.

N-PSDB; AAZ98202.

New human signal peptide-containing proteins useful in treatment,
prevention and diagnosis of e.g. cancer, inflammation and
cardiovascular disease

Claim 1; Page 220-221; 327pp; English.

AAZ98109 to AAZ98242 encode AY87224 to AY87357 which represent the
human signal peptide-containing proteins HSPP-1 to HSPP-134. HSPPs have
anticancer, anti-inflammatory, antimicrobial, nootropic, hepatotropic,
neuroprotective, cardiovascular and antiasthmatic activities, and can
be used in gene therapy. HSPPs can be used to treat or prevent disorders
associated with decreased activity or function of HSPP. Antagonists of
HSPP are used to treat or prevent disorders associated with increased
activity or function of HSPP. Such diseases include cell proliferation
(including cancer), inflammation, cardiovascular, neurological,
reproductive or developmental disorders, (e.g. arteriosclerosis,
cirrhosis, psoriasis, acquired immune deficiency syndrome, anaemia,
asthma, Crohn's disease, microbial or other infections, congestive or
ischaemic heart disease, Alzheimer's, Parkinson's or Huntington's
diseases, schizophrenia, ovulatory defects, muscular dystrophy). HSPP
nucleic acids can be used for the recombinant production of HSPP, for
detecting HSPP in standard hybridisation and amplification assays (for
diagnosis and monitoring), in gene therapy, as antisense,
triplex-forming or ribozyme therapeutics, for detecting related sequences
or genetic variations, and for chromosomal mapping. HSPP are also used to
raise specific antibodies (Ab) and to screen for agonists and
antagonists (potential therapeutic agents). Ab are used to diagnose, or
monitor, HSPP-related diseases (in usual immunoassays), as therapeutic
antagonists, in competitive drug screens, and for purification of HSPP
from natural sources.

Sequence 119 AA;

very Match 100.0%; Score 119, DB 21; Length 119;
est Local Similarity 100.0%; Pred. No. 3.3e-110; Mismatches 0; Gaps 0;
atches 119; Conservative 0; Indels 0;

1 MKVLISLLLLPLMLMSVSSSLNPGVARGHSDRGQASRRWLQEGGQCECKDWFRLAP 60

1 MKVLISLLLLPLMLMSVSSSLNPGVARGHSDRGQASRRWLQEGGQCECKDWFRLAP 60

61 RRKWTWSGLPKQCPDCHFKGNVYKTKTHORHHRKPNKHSRACQQLKQQLRSFALPL 119

61 RRKWTWSGLPKQCPDCHFKGNVYKTKTHORHHRKPNKHSRACQQLKQQLRSFALPL 119

RESULT 4

AAZ98242

ID AAY66668 standard; protein; 119 AA.

XX AAY66668;

AC AAY66668;

XX 05-APR-2000 (first entry)

XX Membrane-bound protein PRO842.

DE Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;

KW pharmaceutical; receptor immunoadhesin; gene mapping.

XX Homo sapiens.

OS WO9963088-A2.

XX 09-DEC-1999.

XX 02-JUN-1999; 99WO-US12252.

XX 02-JUN-1998; 98US-0087607.

PR 02-JUN-1998; 98US-0087609.

PR 02-JUN-1998; 98US-0087759.

PR 03-JUN-1998; 98US-0087827.

PR 04-JUN-1998; 98US-0088021.

PR 04-JUN-1998; 98US-0088025.

PR 04-JUN-1998; 98US-0088028.

PR 04-JUN-1998; 98US-0088029.

PR 04-JUN-1998; 98US-0088030.

PR 04-JUN-1998; 98US-0088033.

PR 04-JUN-1998; 98US-0088326.

PR 05-JUN-1998; 98US-0088167.

PR 05-JUN-1998; 98US-0088202.

PR 05-JUN-1998; 98US-0088212.

PR 05-JUN-1998; 98US-0088217.

PR 09-JUN-1998; 98US-0088655.

PR 10-JUN-1998; 98US-0088722.

PR 10-JUN-1998; 98US-0088730.

PR 10-JUN-1998; 98US-0088734.

PR 10-JUN-1998; 98US-0088738.

PR 10-JUN-1998; 98US-0088740.

PR 10-JUN-1998; 98US-0088741.

PR 10-JUN-1998; 98US-0088742.

PR 10-JUN-1998; 98US-0088810.

PR 10-JUN-1998; 98US-0088811.

PR 10-JUN-1998; 98US-0088824.

PR 10-JUN-1998; 98US-0088825.

PR 10-JUN-1998; 98US-0088826.

PR 11-JUN-1998; 98US-0088858.

PR 11-JUN-1998; 98US-0088861.

PR 11-JUN-1998; 98US-0088863.

PR 11-JUN-1998; 98US-0088876.

PR 12-JUN-1998; 98US-0089090.

PR 12-JUN-1998; 98US-0089105.

PR 16-JUN-1998; 98US-0089440.

PR 16-JUN-1998; 98US-0089512.

PR 16-JUN-1998; 98US-0089514.

PR 17-JUN-1998; 98US-0089532.

PR 17-JUN-1998; 98US-0089538.

PR 17-JUN-1998; 98US-0089598.

PR 17-JUN-1998; 98US-0089600.

PR 17-JUN-1998; 98US-0089653.

PR 18-JUN-1998; 98US-0089801.

PR 18-JUN-1998; 98US-0089907.

PR 18-JUN-1998; 98US-0089908.

PR 19-JUN-1998; 98US-0089947.

PR 19-JUN-1998; 98US-0089948.

PR 19-JUN-1998; 98US-0089952.

PR 22-JUN-1998; 98US-0090246.

PR 22-JUN-1998; 98US-0090252.

PR 22-JUN-1998; 98US-0090254.

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23-JUN-1998; 98US-0090349.
24-JUN-1998; 98US-0090355.
24-JUN-1998; 98US-0090429.
24-JUN-1998; 98US-0090431.
24-JUN-1998; 98US-0090435.
24-JUN-1998; 98US-0090444.
24-JUN-1998; 98US-0090445.
24-JUN-1998; 98US-0090461.
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24-JUN-1998; 98US-0090535.
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24-JUN-1998; 98US-0090540.
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25-JUN-1998; 98US-0090690.
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25-JUN-1998; 98US-0090696.
26-JUN-1998; 98US-0090862.
26-JUN-1998; 98US-0090863.
01-JUL-1998; 98US-0091358.
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01-JUL-1998; 98US-0091544.
02-JUL-1998; 98US-0091478.
02-JUL-1998; 98US-0091486.
02-JUL-1998; 98US-0091519.
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02-JUL-1998; 98US-0091646.
02-JUL-1998; 98US-0091673.
07-JUL-1998; 98US-0091978.
07-JUL-1998; 98US-0091982.
08-JUL-1998; 98US-0092182.
10-JUL-1998; 98US-0092472.
20-JUL-1998; 98US-0093339.
30-JUL-1998; 98US-0094651.
04-AUG-1998; 98US-0095282.
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04-AUG-1998; 98US-0095301.
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10-AUG-1998; 98US-0095916.
10-AUG-1998; 98US-0095929.
10-AUG-1998; 98US-0096012.
11-AUG-1998; 98US-0096143.
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98US-0097978.
98US-0097979.
98US-0097986.
98US-0098014.
98US-0098525.
98US-0100634.
99US-0115565.
XX
XX (GETH ) GENENTECH INC.
PA
XX Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;
PI Wood WI, Yuan J;
XX
XX WPI; 2000-072883/06.
XX N-PSDB; AAZ65001.
XX
XX Membrane-bound proteins and related nucleotide sequences
XX
XX claim 12; Fig 99; 822pp; English.
XX
XX The invention provides membrane-bound PRO polypeptides and
XX polynucleotides encoding them. The PRO sequences of the invention were
XX identified based on extracellular domain homology screening. The PRO
XX sequences have homology with proteins including LDL receptors, TIE
XX ligands and various enzymes. The membrane-bound proteins and receptor
XX molecules are useful as pharmaceutical and diagnostic agents. Receptor
XX immunoadhesins, for instance, can be used as therapeutic agents to block
XX receptor-ligand interactions. The membrane-bound proteins can also be
XX employed for screening of potential peptide or small molecule inhibitors
XX of the relevant receptor/ligand interaction. The PRO encoding sequences
XX are useful as hybridization probes, in chromosome and gene mapping and in
XX the generation of antisense RNA and DNA. PRO nucleic acid sequences
XX will also be useful for the preparation of PRO polypeptides, especially
XX by recombinant techniques.
XX
XX Sequence 119 AA;
XX
XX Query Match 100.0%; Score 119; DB 21; Length 119;
XX Best Local Similarity 100.0%; Pred. No. 3.3e-110;
XX Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 MKVLISLLLLLPLMLMSVSSSLNPGVARGHRDQGASRRWLQEGQCECKDWFLRAP 60
QY 61 RKFMVTVSGLPKKQPCDHFKNVKTTHQHHKPNKHSRACQQLKQCLRSFALPL 119
Db 61 RKFMVTVSGLPKKQPCDHFKNVKTTHQHHKPNKHSRACQQLKQCLRSFALPL 119
RESULT 5
AAU29093
ID AAU29093 standard; Protein; 119 AA.
XX
XX AAU29093;
AC
XX
XX 18-DEC-2001 (first entry)
XX
XX Human PRO polypeptide sequence #70.
XX
XX PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep;
XX dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
XX blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
XX adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.
XX
XX Homo sapiens.
XX
XX WO200168848-A2.
XX
```

20-SEP-2001.

28-FEB-2001; 2001WO-US06520.

01-MAR-2000; 2000WO-US05601.
02-MAR-2000; 2000WO-US05841.
03-MAR-2000; 2000US-187202P.
06-MAR-2000; 2000US-186968P.
14-MAR-2000; 2000US-189320P.
14-MAR-2000; 2000US-189328P.
15-MAR-2000; 2000WO-US06884.
21-MAR-2000; 2000US-190828P.
21-MAR-2000; 2000US-191007P.
21-MAR-2000; 2000US-191048P.
21-MAR-2000; 2000US-191314P.
28-MAR-2000; 2000US-192655P.
29-MAR-2000; 2000US-193032P.
29-MAR-2000; 2000US-193053P.
30-MAR-2000; 2000WO-US08439.
04-APR-2000; 2000US-194443P.
04-APR-2000; 2000US-194647P.
11-APR-2000; 2000US-195975P.
11-APR-2000; 2000US-196000P.
11-APR-2000; 2000US-196187P.
11-APR-2000; 2000US-196690P.
11-APR-2000; 2000US-196820P.
18-APR-2000; 2000US-198121P.
18-APR-2000; 2000US-198585P.
25-APR-2000; 2000US-199397P.
25-APR-2000; 2000US-199550P.
25-APR-2000; 2000US-199654P.
03-MAY-2000; 2000US-201516P.
17-MAY-2000; 2000WO-US13705.
22-MAY-2000; 2000WO-US14042.
30-MAY-2000; 2000WO-US14941.
02-JUN-2000; 2000WO-US15284.
05-JUN-2000; 2000US-209832P.
28-JUL-2000; 2000WO-US20710.
22-AUG-2000; 2000US-0644848.
24-AUG-2000; 2000WO-US23328.
08-NOV-2000; 2000WO-US30952.
01-DEC-2000; 2000WO-US32678.
20-DEC-2000; 2000WO-US34956.

(GETH) GENENTECH INC.

Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;

WPI; 2001-602746/68.
N-PSDB; AAS45994.

Novel nucleic acids encoding PRO polypeptides, used to diagnose the presence of tumours, such as prostate and breast tumours, in mammals and to screen for modulators of the compounds -

Claim 11; Fig 140; 774pp; English.

Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention. The PRO polypeptides and their associated nucleic acids can be used to detect the presence of a tumour in a mammal by comparing the level of expression of a PRO polypeptide in a test sample of cells from the animal and a control sample of normal cells, whereby a higher level of expression in the test sample indicates the presence of a tumour in the mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats and rabbits but are preferably human. The polypeptides can be used to stimulate tumour necrosis factor (TNF) alpha release from human blood, when contacted with it. A specific polypeptide can be used to stimulate the proliferation or differentiation of chondrocyte cells. The PRO proteins can be used to determine the presence of tumours and also susceptibility to tumour development, particularly adrenal, lung, colon, breast, prostate, rectal, cervical, or liver tumours, in mammalian subjects. The oligonucleotide probes specific for the PRO nucleic acids

CC can be used for genetic analysis of individuals with genetic disorders.

SQ Sequence 119 AA;
Query Match 100.0%; Score 119; DB 22; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-110;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKVLISLLLLLPLMLMSVSSSLNPGVARGHRDRGQASRRWLQGGQCECKDWFLRAP 60
DB 1 MKVLISLLLLLPLMLMSVSSSLNPGVARGHRDRGQASRRWLQGGQCECKDWFLRAP 60
QY 61 RRKFTVSGLPKQPCDHFKGNVKTQRHRRKPKHSRACQOFLKQCQLRSFALPL 119
DB 61 RRKFTVSGLPKQPCDHFKGNVKTQRHRRKPKHSRACQOFLKQCQLRSFALPL 119

RESULT 6

RAG63977
ID AAG63977 standard; Protein; 119 AA.

XX AC AAG63977;

XX DT 13-NOV-2001 (first entry)

XX DE Amino acid sequence of a human Lngl04 polypeptide.

XX KW Human; lung cancer specific gene; LSG; Lngl04; lung cancer.

XX OS Homo sapiens.

XX PN WO200161055-A2.

XX PD 23-AUG-2001.

XX PF 20-FEB-2001; 2001WO-US05674.

XX PR 17-FEB-2000; 2000US-0183188.

XX PA (DIAD-) DIADEXUS INC.

XX FI Chen S, Sun Y, Macina RA;

XX DR WPI; 2001-529917/58.

XX DR N-PSDB; AAH77949, AAH77951.

XX PT New lung cancer specific gene for the treatment and diagnosis of lung cancer -

XX FS Claim 2; Page 115-116; 119pp; English.

XX CC The present sequence is encoded by a human lung cancer specific gene (LSG), and represents a polypeptide designated Lngl04. LSGs are useful in the treatment and diagnosis of lung cancer. The treatment of lung cancer comprises the administration of a molecule which down regulates the expression of an LSG. An immune response can be mounted against a target cell expressing an LSG. Identification of potential therapeutic agents for use in imaging and treating lung cancer which comprises screening molecules for an ability to bind to or decrease expression of an LSG relative to LSG in the absence of the agent where the ability of a molecule to bind to the LSG or decrease expression of the LSG is indicative of the molecule being useful in imaging and treating lung cancer.

SQ Sequence 119 AA;
Query Match 100.0%; Score 119; DB 22; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-110;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKVLISLLLLLPLMLMSVSSSLNPGVARGHRDRGQASRRWLQGGQCECKDWFLRAP 60
DB 1 MKVLISLLLLLPLMLMSVSSSLNPGVARGHRDRGQASRRWLQGGQCECKDWFLRAP 60

61 RRKFTVTVGLPKKQPCDHFHKGKGVKTKTHQHRHKKPKNKHSRACQOFLKQCOLRSFALPL 119
 61 RRKFTVTVGLPKKQPCDHFHKGKGVKTKTHQHRHKKPKNKHSRACQOFLKQCOLRSFALPL 119

ULT 7
 387538
 AAB87538 standard; Protein; 119 AA.

AAB87538;

15-MAY-2001 (first entry)

Human PRO842.

Human; PRO protein; mapping.

Homo sapiens.

WO200116318-A2.

08-MAR-2001.

24-AUG-2000; 2000WO-US23328.

01-SEP-1999; 99WO-US20111.
 15-SEP-1999; 99WO-US21090.
 07-DEC-1999; 99US-0169495.
 09-DEC-1999; 99US-0170262.
 11-JAN-2000; 2000US-0175481.
 18-FEB-2000; 2000WO-US04341.
 18-FEB-2000; 2000WO-US04342.
 22-FEB-2000; 2000WO-US04414.
 01-MAR-2000; 2000WO-US05601.
 03-MAR-2000; 2000US-0187202.
 25-APR-2000; 2000US-0199397.
 22-MAY-2000; 2000WO-US14042.
 05-JUN-2000; 2000US-0209832.

(GETH) GENENTECH INC.

Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
 Grimaldi CJ, Gurney AL, Watanabe CK, Wood WI;

WPI; 2001-183260/18.
 N-PSDB; AAF92070.

Eighty four nucleic acids encoding PRO polypeptides, useful in
 molecular biology, including use as hybridization probes, and in
 chromosome and gene mapping.

Claim 12; Fig 26; 278pp; English.

The present sequence is a human PRO polypeptide (secreted and
 transmembrane). The PRO protein, and PRO agonists, PRO antagonists or
 anti-PRO antibodies are useful for preparation of a medicament useful in
 the treatment of a condition which is responsive to the PRO protein,
 agonists, antagonists or anti-PRO antibodies. The PRO protein may also be
 employed as molecular weight markers for protein electrophoresis. The PRO
 coding sequence has applications in molecular biology, including use as
 hybridisation probes, and in chromosome and gene mapping.

Sequence 119 AA;

Query Match 100.0%; Score 119; DB 22; Length 119;

Best Local Similarity 100.0%; Pred. No. 3.3e-110; Indels 0; Gaps 0;

Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MKVLISLLLLPLMLMSVSSSLNFGVARGHRDRGQASRRWLQSGQCECKDWFLRAP 60

1 MKVLISLLLLPLMLMSVSSSLNFGVARGHRDRGQASRRWLQSGQCECKDWFLRAP 60

OY 61 RRKFTVTVGLPKKQPCDHFHKGKGVKTKTHQHRHKKPKNKHSRACQOFLKQCOLRSFALPL 119
 DB 61 RRKFTVTVGLPKKQPCDHFHKGKGVKTKTHQHRHKKPKNKHSRACQOFLKQCOLRSFALPL 119

RESULT 8

AAB65191

ID AAB65191 standard; Protein; 119 AA.

XX AC AAB65191;

XX 02-APR-2001 (first entry)

XX Human PRO842 (UNQ473) protein sequence SEQ ID NO:165.

XX Human; secreted and transmembrane protein; PRO; cytostatic;
 KW cell death; cancer; chromosomal mapping; gene mapping; tissue typing;
 KW diagnostic assay.

XX Homo sapiens.

XX WO2000073454-A1.

XX 07-DEC-2000.

XX 30-MAR-2000; 2000WO-US08439.

XX 02-JUN-1999; 99WO-US12252.
 PR 23-JUN-1999; 99US-0141037.
 PR 07-JUL-1999; 99US-0143048.
 PR 20-JUL-1999; 99US-0144758.
 PR 26-JUL-1999; 99US-0145698.
 PR 28-JUL-1999; 99US-0146222.
 PR 17-AUG-1999; 99US-0149396.
 PR 15-SEP-1999; 99WO-US21090.
 PR 15-SEP-1999; 99WO-US21547.
 PR 08-OCT-1999; 99US-0159663.
 PR 30-NOV-1999; 99WO-US28313.
 PR 01-DEC-1999; 99WO-US28301.
 PR 16-DEC-1999; 99WO-US30095.
 PR 20-DEC-1999; 99WO-US30911.
 PR 05-JAN-2000; 2000WO-US00219.
 PR 06-JAN-2000; 2000WO-US00376.
 PR 11-FEB-2000; 2000WO-US03565.
 PR 18-FEB-2000; 2000WO-US04341.
 PR 22-FEB-2000; 2000WO-US04414.
 PR 24-FEB-2000; 2000WO-US04914.
 PR 24-FEB-2000; 2000WO-US05004.
 PR 02-MAR-2000; 2000WO-US05841.
 PR 15-MAR-2000; 2000WO-US06884.
 PR 20-MAR-2000; 2000WO-US07377.

XX (GETH) GENENTECH INC.

XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
 PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi CJ, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;
 PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
 PI Zhang Z;

XX WPI; 2001-032160/04.
 DR N-PSDB; AAF44147.

XX PRO polynucleotides used to produce polypeptides used to target
 PT bioactive molecules such as toxins, radiolabels or antibodies, to
 PT specific cells, to cause targeted cell death -

XX Claim 12; Fig 99; 935pp; English.

XX The present invention describes human secreted and transmembrane PRO
 CC proteins. The PRO proteins have cytostatic activity. The PRO proteins
 CC can be used for targeted delivery of bioactive molecules, such as
 CC toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide

sequences, and their fragments, can be used as hybridisation probes, in chromosomal and gene mapping, and in the generation of anti-sense RNA and DNA. They may also be used to produce transgenic animals which are used to develop and screen therapeutically useful reagents. The PRO nucleotide and protein sequence can be used for tissue typing and in treating cancer. Anti-PRO antibodies can be used in diagnostic assays. AAF44270 to AAF44470 represent PCR primers and hybridisation probes used in the isolation of human PRO sequences. AAF44087 to AAF44269 and AAB65154 to AAB65300 represent human PRO polynucleotide and protein sequences given in the exemplification of the present invention.

Sequence 119 AA;

Query March 100.0%; Score 119; DB 22; Length 119;
 Best Local Similarity 100.0%; Pred. No. 3.3e-110; Indels 0; Gaps 0;
 Matches 119; Conservative 0; Mismatches 0;
 1 MKVLISLLLLPLMLMSVSSSLNPGVARGHRDRGQASRRWLQEGGQCECKDWFLRAP 60
 1 MKVLISLLLLPLMLMSVSSSLNPGVARGHRDRGQASRRWLQEGGQCECKDWFLRAP 60
 61 RRKPMVTSGLPKKQCPDHFPGKGVKTRHQRHRRKPKHRSRACQQLKQCLRSFALPL 119
 61 RRKPMVTSGLPKKQCPDHFPGKGVKTRHQRHRRKPKHRSRACQQLKQCLRSFALPL 119

JLT 9

54931

ABP54931 standard; Protein; 119 AA.

ABP54931;

08-JAN-2003 (first entry)

Human cytokine PRO842 (CK27).

PRO842; CK27; chemokine; human; antiinflammatory; dermatological;
 hepatotropic; anti-allergic; antiasthmatic; immunosuppressive;
 antithyroid; antidiabetic; antianaemic; haemostatic; antipsoriatic;
 antirheumatic; antiarthritic; nephrotropic.

Homo sapiens.

Key Location/Qualifiers
 Peptide 1..22
 Protein 23..119
 Modified-site 27..32
 Modified-site 39..41
 Modified-site 46..51
 /label= Signal_peptide
 /label= Mature_protein
 /note= "potential N-myristoylation site"
 /note= "potential protein kinase C phosphorylation site"
 /note= "potential N-myristoylation site"

WO200270706-A2.

12-SEP-2002.

07-DEC-2001; 2001WO-US48060.

28-FEB-2001; 2001WO-US06520.

28-AUG-2001; 2001US-0941992.

(GETH) GENENTECH INC.

French D, Grimaldi JC, Hilian KJ, Pisabarro MT, Schmidt KN,
 Smith V, Tumas D, Vandlen RL, Watanabe CK, Williams PM, Wood WT;

WPI: 2002-750461/81.

N-PSDB; ABV73914.

PT New PRO842 polypeptides having structural homology to interleukin-8,
 PT useful for treating or diagnosing a mammal with an inflammatory disease
 PT or immune related disease, e.g. rheumatoid arthritis, osteoarthritis or
 PT allergic disease .

XX Claim 1; Fig 2; 118pp; English.

XX The present sequence is the protein sequence of PRO842 (CK27),
 CC a novel human chemokine (mol.wt. 13.8 kDa, pI 11.16) having
 CC structural homology to interleukin-8. Microarray analysis has
 CC shown PRO842 to be over-expressed in colon tumour, lung tumour and
 CC breast tumour cells compared with non-cancerous human tissue,
 CC making it a useful diagnostic marker for cancerous tumours and a
 CC therapeutic target. PRO842 also plays a role in the inflammatory
 CC response, having chemottractant properties toward monocytes and
 CC dendritic cells. The invention provides PRO842 polypeptides,
 CC polynucleotides, host cells, vectors and antibodies, as well as
 CC methods of treating an immune related disorder by using a PRO842
 CC polypeptide, or an agonist, antagonist or antibody. The immune
 CC related disorder may be systemic lupus erythematosus, rheumatoid
 CC arthritis, osteoarthritis, juvenile chronic arthritis,
 CC spondyloarthritis, systemic sclerosis, idiopathic inflammatory
 CC myopathy, Sjogren's syndrome, systemic vasculitis, sarcoidosis,
 CC autoimmune haemolytic anaemia, autoimmune thrombocytopaenia,
 CC thyroiditis, diabetes mellitus, immune-mediated renal disease,
 CC demyelinating disease of the central or peripheral nervous system,
 CC idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome,
 CC chronic inflammatory demyelinating polyneuropathy, hepatobiliary
 CC disease, infectious or autoimmune chronic active hepatitis, primary
 CC biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,
 CC inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's
 CC disease, an autoimmune or immune-mediated skin disease, a bullous
 CC skin disease, erythema multiforme, contact dermatitis, psoriasis,
 CC an allergic disease, asthma, allergic rhinitis, atopic dermatitis,
 CC food hypersensitivity, urticaria, an immunologic disease of the
 CC ovaries, an immunologic disease of the lung, eosinophilic
 CC pneumonia, idiopathic pulmonary fibrosis, hypersensitivity
 CC pneumonitis, a transplantation associated disease, graft rejection
 CC or graft-versus-host-disease (all claimed).

Sequence 119 AA;

Query Match 100.0%; Score 119; DB 23; Length 119;
 Best Local Similarity 100.0%; Pred. No. 3.3e-110; Indels 0; Gaps 0;
 Matches 119; Conservative 0; Mismatches 0;
 QY 1 MKVLISLLLLPLMLMSVSSSLNPGVARGHRDRGQASRRWLQEGGQCECKDWFLRAP 60
 DB 1 MKVLISLLLLPLMLMSVSSSLNPGVARGHRDRGQASRRWLQEGGQCECKDWFLRAP 60
 QY 61 RRKPMVTSGLPKKQCPDHFPGKGVKTRHQRHRRKPKHRSRACQQLKQCLRSFALPL 119
 DB 61 RRKPMVTSGLPKKQCPDHFPGKGVKTRHQRHRRKPKHRSRACQQLKQCLRSFALPL 119

RESULT 10

ABG95863

ID ABG95863 standard; Protein; 119 AA.

XX ABG95863;

XX 10-DEC-2002 (first entry)

XX Human secreted/transmembrane protein PRO842.

XX Human; secreted protein; transmembrane protein; antirheumatic;
 KW antiarthritic; osteopathic; sports-related joint problem;
 KW articular cartilage defect; osteoarthritis; rheumatoid arthritis.
 XX Homo sapiens.

XX US2002119130-A1.

XX

29-AUG-2002.

06-DEC-2001; 2001US-0006967.

29-OCT-1997; 97US-063435P.

29-OCT-1997; 97US-064215P.

22-APR-1998; 98US-082797P.

29-APR-1998; 98US-083495P.

15-MAY-1998; 98US-085579P.

10-JUN-1998; 98US-088811P.

10-JUN-1998; 98US-088824P.

11-JUN-1998; 98US-088863P.

12-JUN-1998; 98US-089105P.

16-JUN-1998; 98US-089514P.

16-SEP-1998; 98WO-US19330.

08-MAR-1999; 99WO-US05028.

14-MAY-1999; 99WO-US10733.

02-JUN-1999; 99WO-US12252.

01-SEP-1999; 99WO-US20111.

15-SEP-1999; 99WO-US21090.

15-SEP-1999; 99WO-US21194.

22-DEC-1999; 99WO-US30720.

18-FEB-2000; 2000WO-US04341.

18-FEB-2000; 2000WO-US04342.

30-MAR-2000; 2000WO-US08439.

22-MAY-2000; 2000WO-US14042.

02-JUN-2000; 2000WO-US15264.

23-AUG-2000; 2000WO-US23522.

24-AUG-2000; 2000WO-US23528.

10-NOV-2000; 2000WO-US30873.

01-DEC-2000; 2000WO-US32378.

20-DEC-2000; 2000WO-US34956.

28-FEB-2001; 2001WO-US06520.

20-JUN-2001; 2001WO-US19692.

29-JUN-2001; 2001WO-US21066.

09-JUL-2001; 2001WO-US21735.

(GETH) GENENTECH INC.

Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ,

Grimaldi JC, Gurney AL, Watanabe CK, Wood WI,

WPI; 2002-731348/79.

N-PSDB; ABS74390.

New isolated secreted and transmembrane PRO polypeptide useful for modulating biological activity of a cell, or for treating sports-related joint problems, osteoarthritis or rheumatoid arthritis

Claim 20; Fig 26; 399pp; English.

The invention relates to an isolated secreted and transmembrane PRO polypeptide having 80 % sequence identity to a sequence appearing as AEG95951-ABG95934 or their associated signal peptide, or a sequence of an extracellular domain of the proteins with their associated signal peptide or lacking its associated signal peptide. Also included are the nucleic acids encoding the proteins, vectors, host cells, fusion proteins and antibodies which specifically bind to the proteins. The proteins are useful for detecting a polypeptide designated as A, B, C or D in a sample suspected of containing an A, B, C or D polypeptide, by contacting the sample with a polypeptide designated as E, F, G, H or I (or vice versa) and determining the formation of a A/E, B/F, C/H or D/I polypeptide conjugate in the sample, where the formation of the conjugate is indicative of the presence of an A, B, C or D polypeptide in the sample, where A is a PRO10272 polypeptide, B is a PRO20110 polypeptide, C is a PRO10096 polypeptide, D is a PRO19760 polypeptide, E is a PRO5801 polypeptide, F is a PRO1 polypeptide, G is a PRO20040 polypeptide, H is a PRO20233 polypeptide and I is a PRO1890 polypeptide. The sample comprises a cell suspected of expressing the A, B, C or D polypeptide. The E, F, G, H or I polypeptide is labeled with a detectable label or is attached to a solid support. The proteins are useful for linking a bioactive molecule to a cell expressing a

CC polypeptide designated as A, B, C or D or E, F, G, H or I. The bioactive molecule is a toxin, a radiolabel or an antibody. The bioactive molecule causes death of the cell. A, B, C, D, E, F, G, H, or I, or antibodies against them are useful for modulating a biological activity of a cell expressing a polypeptide designated as A, B, C or D or E, F, G, H, or I. The cell is killed. The proteins are useful for identifying agonists or antagonists, for the preparation of a medicament useful in the treatment of a condition which is responsive to the proteins, and as molecular weight markers for protein electrophoresis purposes, and as therapeutic agents for treating sports-related joint problems, articular cartilage defects, osteoarthritis or rheumatoid arthritis. CC Nucleic acids encoding the proteins are useful as hybridisation probes, in chromosome and gene mapping, in the generation of anti-sense RNA and DNA, for the preparation of the proteins, to generate transgenic or knockout animals which are useful in the development and screening of therapeutic useful reagents, for chromosome identification, and in gene therapy. The antibody is useful as a therapeutic agent, in a diagnostic assay and for affinity purification of the protein from recombinant cell culture natural sources. The present sequence represents a novel secreted or transmembrane protein of the invention.

XX Sequence 119 AA;

Query Match 100.0%; Score 119; DB 23; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-110;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKVLISLLLLPLMLSMVSSSLNPGVAGHGRDQASRRWLQEGGQCECKDWFRLAP 60

DB 1 MKVLISLLLLPLMLSMVSSSLNPGVAGHGRDQASRRWLQEGGQCECKDWFRLAP 60

QY 61 RRKMTVSGLPKQPCDHPKGNVKTTRHQRHHRKPNKHSRACQQLKQCLRSFALPL 119

DB 61 RRKMTVSGLPKQPCDHPKGNVKTTRHQRHHRKPNKHSRACQQLKQCLRSFALPL 119

RESULT 11

ABU71181
ID ABU71181 standard; Protein; 119 AA.

XX AC ABU71181;

DT 10-JUN-2003 (first entry)

XX DE Human PRO842 protein.

XX Human; PRO; secreted; transmembrane; cytostatic; TNF-alpha; blood;
KW tumour necrosis factor alpha release; chondrocyte cell; proliferation;
KW differentiation; tumour; gene therapy.

XX Homo sapiens.

XX US2003036143-A1.

XX 20-FEB-2003.

PF 02-JUL-2002; 2002US-0187600.

PR 16-SEP-1998; 98WO-US19330.

PR 07-OCT-1998; 98WO-US21141.

PR 01-DEC-1998; 98WO-US25108.

PR 08-MAR-1999; 99WO-US05028.

PR 14-MAY-1999; 99WO-US10733.

PR 02-JUN-1999; 99WO-US12252.

PR 01-SEP-1999; 99WO-US20111.

PR 15-SEP-1999; 99WO-US21090.

PR 01-DEC-1999; 99WO-US28301.

PR 02-DEC-1999; 99WO-US28551.

PR 30-DEC-1999; 99WO-US31274.

PR 05-JAN-2000; 2000WO-US00219.

PR 18-FEB-2000; 2000WO-US04341.

PR 18-FEB-2000; 2000WO-US04342.

PR 22-FEB-2000; 2000WO-US04414.

24-FEB-2000;	2000WO-US05004.	PR	15-MAY-1998;	98US-085700P.
01-MAR-2000;	2000WO-US05601.	PR	18-MAY-1998;	98US-086023P.
02-MAR-2000;	2000WO-US05841.	PR	22-MAY-1998;	98US-086392P.
15-MAR-2000;	2000WO-US06884.	PR	22-MAY-1998;	98US-086486P.
30-MAR-2000;	2000WO-US08439.	PR	28-MAY-1998;	98US-087098P.
17-MAY-2000;	2000WO-US13705.	PR	28-MAY-1998;	98US-087208P.
22-MAY-2000;	2000WO-US14042.	PR	02-JUN-1998;	98US-087609P.
30-MAY-2000;	2000WO-US14941.	PR	02-JUN-1998;	98US-087759P.
02-JUN-2000;	2000WO-US15264.	PR	03-JUN-1998;	98US-087827P.
28-JUL-2000;	2000WO-US23710.	PR	04-JUN-1998;	98US-088025P.
24-AUG-2000;	2000WO-US23328.	PR	04-JUN-1998;	98US-088028P.
08-NOV-2000;	2000WO-US30952.	PR	04-JUN-1998;	98US-088029P.
01-DEC-2000;	2000WO-US32678.	PR	04-JUN-1998;	98US-088033P.
20-DEC-2000;	2000WO-US34956.	PR	04-JUN-1998;	98US-088326P.
28-FEB-2001;	2001WO-US06520.	PR	05-JUN-1998;	98US-088167P.
01-JUN-2001;	2001WO-US17800.	PR	05-JUN-1998;	98US-088202P.
20-JUN-2001;	2001WO-US19692.	PR	05-JUN-1998;	98US-088212P.
29-JUN-2001;	2001WO-US21062.	PR	05-JUN-1998;	98US-088217P.
09-JUL-2001;	2001WO-US21735.	PR	09-JUN-1998;	98US-088555P.
29-AUG-2001;	2001WO-US27099.	PR	10-JUN-1998;	98US-088722P.
18-SEP-1997;	97US-059263P.	PR	10-JUN-1998;	98US-088738P.
18-SEP-1997;	97US-059266P.	PR	10-JUN-1998;	98US-088740P.
17-OCT-1997;	97US-062250P.	PR	10-JUN-1998;	98US-088811P.
21-OCT-1997;	97US-063486P.	PR	10-JUN-1998;	98US-088824P.
24-OCT-1997;	97US-063120P.	PR	10-JUN-1998;	98US-088825P.
24-OCT-1997;	97US-063121P.	PR	10-JUN-1998;	98US-088826P.
28-OCT-1997;	97US-063340P.	PR	11-JUN-1998;	98US-088861P.
28-OCT-1997;	97US-063341P.	PR	11-JUN-1998;	98US-088863P.
28-OCT-1997;	97US-063544P.	PR	11-JUN-1998;	98US-088876P.
28-OCT-1997;	97US-063564P.	PR	12-JUN-1998;	98US-089090P.
29-OCT-1997;	97US-063734P.	PR	12-JUN-1998;	98US-089105P.
31-OCT-1997;	97US-063870P.	PR	16-JUN-1998;	98US-089512P.
31-OCT-1997;	97US-064103P.	PR	16-JUN-1998;	98US-089514P.
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02-SEP-1998; 98US-098843P.
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RULT 12
J71518
ASU71518 standard; Protein; 119 AA.
ABU71518;
10-JUN-2003 (first entry)
Human secreted polypeptide PRO842.
Human; gene therapy; tumour; cancer.
Homo sapiens.
US2003013855-A1.
16-JAN-2003.
03-MAY-2002; 2002US-0063616.
30-DEC-1998; 98RX-0062142.
08-MAR-1999; 99WO-USC05028.
14-MAY-1999; 99WO-US10733.
30-DEC-1999; 99WO-US31274.
18-FEB-2000; 2000WO-USC04341.
01-MAR-2000; 2000WO-USC5601.
02-MAR-2000; 2000WO-USC05841.
21-MAR-2000; 2000WO-US07532.
22-MAY-2000; 2000WO-US14042.
03-JUN-2000; 2000WO-US15264.
24-AUG-2000; 2000WO-US23328.
10-NOV-2000; 2000WO-US30873.
01-DEC-2000; 2000WO-US32878.
20-DEC-2000; 2000WO-US34956.
28-FEB-2001; 2001WO-USC06520.
01-JUN-2001; 2001WO-US17800.
14-MAY-1999; 99US-0311832.
25-AUG-1999; 99US-0380137.
25-AUG-1999; 99US-0380138.
25-AUG-1999; 99US-0380139.
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25-AUG-1999; 99US-0380142.
15-SEP-1999; 99US-0397342.
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12-NOV-1999; 99US-0423844.
22-AUG-2000; 2000US-0644848.
18-SEP-2000; 2000US-0644610.
18-SEP-2000; 2000US-0685350.
08-NOV-2000; 2000US-0709238.
20-DEC-2000; 2000US-0747259.
22-MAR-2001; 2001US-0816744.
10-MAY-2001; 2001US-0854208.
30-MAY-2001; 2001US-0870574.
05-JUN-2001; 2001US-0874503.
29-JUN-2001; 2001US-0865599.
18-JUL-2001; 2001US-0908827.
06-DEC-2001; 2001US-0906867.

XX (GETH ) GENENTECH INC.
XX
XX Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
XX
XX WPI; 2003-330485/31.
XX N-PSDB; ACA58822.
XX
XX New isolated antibody specifically binding a PRO polypeptide, useful
PT for the preparation of a medicament for treating disorders with the
PT aberrant expression or activity of the PRO polypeptide, such as tumor
XX conditions and cancer
XX
XX Disclosure; Page 93; 406pp; English.
XX
XX The invention relates to an antibody that binds to a polypeptide with a
CC fully defined sequence given in the specification. The methods and
CC compositions (containing antibodies that specifically bind a PRO
CC polypeptide) of the present invention are useful for the preparation of a
CC medicament for the treatment of disorders associated with the aberrant
CC expression or activity of the PRO polypeptide, such as tumour conditions
CC and cancer. They can also be used to generate transgenic or knockout
CC animals useful in the development and screening of therapeutically useful
CC reagents. The PRO polypeptides and encoding nucleic acids can be used as
CC molecular weight markers for protein electrophoresis, chromosome
CC identification and tissue typing. The PRO polypeptides are useful to
CC induce angiogenesis e.g wound healing; in the treatment of sports-related
CC joint problems, articular cartilage defects, osteoarthritis or rheumatoid
CC arthritis; diabetes; hyperinsulinaemia and hypoinsulinaemia. The
CC antibodies may be used in various diagnostic, competitive binding and/or
CC immunoprecipitation assays. The present sequence represents the amino
CC acid sequence of a PRO polypeptide of the invention.
XX
XX Sequence 119 AA;

Query Match 100.0%; Score 119; DB 24; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-110;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MKVLISSLLLLPLMLMSVSSSLNPGVARGHRRDGRQASRRWLQEGGQCECKDWFRLAP 60
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DB 61 RRKFMVTSGLPKQCPCHDFKGNVKTTHQHHKPNKHSRACQOFLKQCQLRSFALPL 119

RESULT 13
ABU71964
ID ABU71964 standard; Protein; 119 AA.
XX
XX AC ABU71964;
XX
XX DT 11-JUN-2003 (first entry)
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Novel human secreted and transmembrane protein PRO842.

Human; secreted and transmembrane polypeptide;
chromosome mapping; gene mapping; transgenic animal; knockout animal;
therapeutic agent screening; chromosome identification; tissue typing;
gene therapy.

Homo sapiens.

US2003018183-A1.

23-JAN-2003.

01-MAY-2002; 2002US-0063512.

06-DEC-2001; 2001US-0006867.

(GETH) GENENTECH INC.

Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;

WPI; 2003-330984/31.
N-PSDB; ACA60375.

New secreted and transmembrane PRO polypeptides and nucleic acid
molecules encoding the polypeptides, useful in gene therapy or
preparing a medicament for treating a condition that is responsive to
the PRO polypeptide or antibody -

Disclosure; Fig 26; 409pp; English.

The invention describes novel isolated PRO polypeptides. The PRO
polypeptides or anti-PRO antibodies are useful in preparing a medicament
for treating a condition that is responsive to the PRO polypeptide or
antibody. The PRO nucleotide sequences may be used as hybridisation
probes in chromosome and gene mapping, or in generating antisense RNA
and DNA. PRO nucleic acids are also useful in preparing PRO polypeptides,
in assays to identify other proteins or molecules involved in binding
reaction, to generate transgenic animals or knockout animals, which in
turn are useful in the development and screening of therapeutically
useful reagents, for chromosome identification, and tissue typing. The
PRO polypeptides and nucleic acid molecules are also useful in gene
therapy, and as molecular weight markers for protein electrophoresis
purposes. The anti-PRO antibodies may be used in diagnostic assays for
PRO, or for the affinity purification of PRO from recombinant cell
culture or natural sources. This is the amino acid sequence of a novel
human secreted and transmembrane PRO polypeptide.

Sequence 119 AA;

Query Match 100.0%; Score 119; DB 24; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-110;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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JLT 14
72121

ABU72121 standard; Protein; 119 AA.

ABU72121;

13-JUN-2003 (first entry)

Human PRO polypeptide #13.

Human; PRO polypeptide; secreted and transmembrane protein;
anti-PRO antibody; diagnostic assay; gene expression.

Homo sapiens.

US2003023042-A1.

30-JAN-2003.

01-MAY-2002; 2002US-0063502.

06-DEC-2001; 2001US-0006867.

(GETH) GENENTECH INC.

Baton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;

WPI; 2003-331484/31.
N-PSDB; ACA63385.

Novel monoclonal antibody that binds to secreted and transmembrane
polypeptide, useful for detecting and purifying the polypeptide and
also for treating conditions responsive to the antibody -

Disclosure; Fig 26; 409pp; English.

The present invention relates to the isolation of novel human PRO
polypeptides, and the polynucleotide sequences encoding them. The
PRO polypeptides are secreted and transmembrane proteins. The PRO
polypeptides and polynucleotides are useful for preparing a
medicament useful in the treatment of a condition responsive to
anti-PRO antibody. Anti-PRO antibodies are useful in diagnostic
assays for PRO, by detecting its expression in specific cells,
tissues or serum, and for affinity purification of PRO from
recombinant cell culture or natural sources. ABU72109-ABU72192
represent the human PRO polypeptides of the invention.

Sequence 119 AA;

Query Match 100.0%; Score 119; DB 24; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-110;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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61 RRKFTVSGLPKQPCDHFKNVKKTRHQRHHRKPNKHSRACQOFLKQCQLRSFALPL 119

RESULT 15

ABU65638

ID ABU65638 standard; Protein; 119 AA.

XX AC ABU65638;

XX DT 19-MAY-2003 (first entry)

XX DE Human secreted/transmembrane protein, SEQ ID 140.

XX KW Human; PRO; secreted protein; transmembrane protein;
cytostatic; antiarthritis; osteopathic; adrenal tumour; lung tumour;
colon tumour; breast tumour; prostate tumour; rectal tumour;
cervical tumour; liver tumour; TNF-alpha release; arthritis;
tumour necrosis factor alpha; chondrocyte cell; bone disorder;
cartilage disorder; sports injury.

XX OS Homo sapiens.

US2003036156-A1.
20-FEB-2003.
02-JUL-2002; 2002US-0188767.
16-SEP-1998; 98WO-US19330.
07-OCT-1998; 98WO-US21141.
01-DEC-1998; 98WO-US25108.
08-MAR-1999; 98WO-US05028.
14-MAY-1999; 98WO-US10733.
02-JUN-1999; 98WO-US1252.
01-SEP-1999; 99WO-US20111.
15-SEP-1999; 99WO-US21090.
01-DEC-1999; 99WO-US28301.
02-DEC-1999; 99WO-US28551.
05-DEC-1999; 99WO-US31274.
30-JAN-2000; 2000WO-US00219.
18-FEB-2000; 2000WO-US04341.
18-FEB-2000; 2000WO-US04342.
22-FEB-2000; 2000WO-US04414.
24-FEB-2000; 2000WO-US05004.
01-MAR-2000; 2000WO-US05601.
02-MAR-2000; 2000WO-US05841.
15-MAR-2000; 2000WO-US06884.
20-MAR-2000; 2000WO-US08439.
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22-MAY-2000; 2000WO-US14042.
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02-JUN-2000; 2000WO-US15264.
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08-NOV-2000; 2000WO-US30952.
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20-DEC-2000; 2000WO-US34956.
28-FEB-2001; 2001WO-US06520.
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Time : 45 secs

GenCore version 5.1.6
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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6	8	6.7	571	4	US-09-134-001C-3865
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8	8	6.7	1023	2	US-08-475-891A-2
9	8	6.7	1023	2	US-08-567-375-2
10	8	6.7	1023	2	US-08-587-680A-2
11	7	5.9	31	1	US-08-090-036-1
12	7	5.9	38	4	US-09-390-134B-34
13	7	5.9	54	4	US-09-227-357-212
14	7	5.9	116	1	US-08-434-705B-6
15	7	5.9	116	2	US-09-086-201-6
16	7	5.9	129	1	US-08-434-705B-4
17	7	5.9	129	2	US-09-086-201-4
18	7	5.9	209	1	US-08-455-001-2
19	7	5.9	209	3	US-08-308-814-2
20	7	5.9	209	4	US-09-214-631-6
21	7	5.9	209	5	PCT-US95-11869-2
22	7	5.9	213	1	US-09-608-324A-10
23	7	5.9	213	2	US-08-920-440B-10
24	7	5.9	213	3	US-09-173-432-10
25	7	5.9	213	4	US-09-173-133-10
26	7	5.9	213	4	US-09-580-236A-10
27	7	5.9	230	2	US-08-471-371-2

Sequence 7, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 6, Appli
Sequence 16901, A
Sequence 2, Appli
Sequence 2, Appli
Sequence 22552, A
Sequence 27879, A
Sequence 4, Appli
Sequence 2, Appli
Sequence 5, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 18540, A

ALIGNMENTS

RESULT 1

US-09-996-243-165

; Sequence 165, Application US/09996243

; Patent No. 6478825

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Kijavini, Ivar J.

; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tamas, Daniel

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; FILE REFERENCE: P2730P1C13

; CURRENT APPLICATION NUMBER: US/09/996,243

; CURRENT FILING DATE: 2001-11-14

; PRIOR APPLICATION NUMBER: 60/049787

; PRIOR FILING DATE: 1997-06-15

; PRIOR APPLICATION NUMBER: 60/062250

; PRIOR FILING DATE: 1997-10-17

; PRIOR APPLICATION NUMBER: 60/065186

; PRIOR FILING DATE: 1997-11-12

; PRIOR APPLICATION NUMBER: 60/065311

; PRIOR FILING DATE: 1997-11-13

; PRIOR APPLICATION NUMBER: 60/066770

; PRIOR FILING DATE: 1997-11-24

; PRIOR APPLICATION NUMBER: 60/075945

; PRIOR FILING DATE: 1998-02-25

; PRIOR APPLICATION NUMBER: 60/078910

; PRIOR FILING DATE: 1998-03-20

; PRIOR APPLICATION NUMBER: 60/083322

; PRIOR FILING DATE: 1998-04-28

[illegible]

PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

very Match 100.0%; Score 119; DB 4; Length 119;
Best Local Similarity 100.0%; Pred. No. 4.3e-108;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MKVLISLILLLPLMLSMVSSSLNPGVARGHRDRGOASRWLQEGQCECKDMLRAP 60
|||||
1 MKVLISLILLLPLMLSMVSSSLNPGVARGHRDRGOASRWLQEGQCECKDMLRAP 60
|||||
61 RRKFTMTVSLPKKQPCDHPKNGVYKTRHQRHHRKPNKHSRACQQLKQCQLRSFALPL 119
|||||
61 RRKFTMTVSLPKKQPCDHPKNGVYKTRHQRHHRKPNKHSRACQQLKQCQLRSFALPL 119
|||||

ULT 2

08-171-299B-9
sequence 9, Application US/08171299B
atent No. 5599665

GENERAL INFORMATION:

APPLICANT: Barbieri, Joseph T.
APPLICANT: Frank, Dara W.
TITLE OF INVENTION: EXOENZYME S PROTEIN PREPARATION AND CLONED EXOENZYME S

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESSEE: QUARLES & BRADY

STREET: 411 East Wisconsin Avenue

CITY: Milwaukee

STATE: Wisconsin

COUNTRY: U.S.A.

ZIP: 53202-4497

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/171,299B

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Baker, Jean C.

REGISTRATION NUMBER: 35,433

REFERENCE/DOCKET NUMBER: 650053.90871

TELECOMMUNICATION INFORMATION:

TELEPHONE: (414) 277-5709

TELEFAX: (414) 271-3552

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 20 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

08-171-299B-9

very Match 6.7%; Score 8; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.37;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

23 SLNPGVAR 30

|||||

13 SLNPGVAR 20

ULT 3

09-461-325-484

sequence 484, Application US/09461325A

; Patent No. 6475753
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 94 Human Secreted Proteins
; FILE REFERENCE: P2029P1
; CURRENT APPLICATION NUMBER: US/09/461,325A
; CURRENT FILING DATE: 1999-12-14
; EARLIER APPLICATION NUMBER: PCT/US99/13418
; EARLIER FILING DATE: 1999-06-15
; EARLIER APPLICATION NUMBER: 60/089,507
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: 60/089,508
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: 60/089,509
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: 60/089,510
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: 60/090,112
; EARLIER FILING DATE: 1998-06-22
; EARLIER APPLICATION NUMBER: 60/090,113
; EARLIER FILING DATE: 1998-06-22
; NUMBER OF SEQ ID NOS: 532
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 484
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (84)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-461-325-484

Query Match 6.7%; Score 8; DB 4; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 SLILLPL 14

|||||

Db 24 SLILLPL 31

RESULT 4

US-08-786-231A-15

; Sequence 15, Application US/08786231A

; Patent No. 6019974

; GENERAL INFORMATION:

; APPLICANT: L'Hernault, Steven W.

; TITLE OF INVENTION: SPE-4 RELATED PEPTIDES, ANTIBODIES AND

; METHOD

; NUMBER OF SEQUENCES: 20

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.

; STREET: 5370 Manhattan Circle, Suite 201

; CITY: Boulder

; STATE: Colorado

; COUNTRY: US

; ZIP: 80303

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/786,231A

; FILING DATE: 24-JAN-1997

; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/010,672

; FILING DATE: 26-JAN-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Ferber, Donna M.

; REGISTRATION NUMBER: 33,878

REFERENCE/DOCKET NUMBER: 60-95

TELECOMMUNICATION INFORMATION:

TELEPHONE: (303) 499-8080

TELEFAX: (303) 499-8089

INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:

LENGTH: 462 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: not relevant

MOLECULE TYPE: protein

HYPOTHETICAL: YES

08-788-231A-15

Query Match 6.7%; Score 8; DB 3; Length 462;

Best Local Similarity 100.0%; Pred. No. 6.2;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

4 LLSLLLLL 11

|||||

162 LLSLLLLL 169

SULT 5

-09-252-991A-22807

Sequence 22807, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 22807

LENGTH: 472

TYPE: PRT

ORGANISM: Pseudomonas aeruginosa

-09-252-991A-22807

Query Match

6.7%; Score 8; DB 4; Length 472;

Best Local Similarity 100.0%; Pred. No. 6.3;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

23 SLNPGVAR 30

|||||

364 SLNPGVAR 371

SULT 6

-09-134-001C-3865

Sequence 3865, Application US/09134001C

Patent No. 6380370

GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS

TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: GTC-007

CURRENT APPLICATION NUMBER: US/09/134,001C

CURRENT FILING DATE: 1998-08-13

PRIOR APPLICATION NUMBER: US 60/064,964

PRIOR FILING DATE: 1997-11-08

PRIOR APPLICATION NUMBER: US 60/055,779

PRIOR FILING DATE: 1997-08-14

NUMBER OF SEQ ID NOS: 5674

SEQ ID NO 3865

LENGTH: 571

TYPE: PRT

ORGANISM: Staphylococcus epidermidis

US-09-134-001C-3865

Query Match

6.7%; Score 8; DB 4; Length 571;

Best Local Similarity 100.0%; Pred. No. 7.5;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LLSLLLLL 11

|||||

Db 556 LLSLLLLL 563

RESULT 7

US-09-285-385C-2

Sequence 2, Application US/09285385C

Patent No. 6579702

GENERAL INFORMATION:

APPLICANT: Greenspan, Daniel S.

APPLICANT: Scott, Ian C.

APPLICANT: Thomas, Christina L.

TITLE OF INVENTION: MAMMALIAN TOLLOID-LIKE GENE AND PROTEIN

FILE REFERENCE: 960296.96111

CURRENT APPLICATION NUMBER: US/09/285,385C

CURRENT FILING DATE: 1999-04-02

PRIOR APPLICATION NUMBER: 60/111873

PRIOR FILING DATE: 1998-12-11

PRIOR APPLICATION NUMBER: 60/080550

PRIOR FILING DATE: 1998-04-03

NUMBER OF SEQ ID NOS: 22

SOFTWARE: Patent In Ver. 2.0

SEQ ID NO 2

LENGTH: 1015

TYPE: PRT

ORGANISM: human

US-09-285-385C-2

Query Match

6.7%; Score 8; DB 4; Length 1015;

Best Local Similarity 100.0%; Pred. No. 13;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 SLLLLLPL 14

|||||

Db 12 SLLLLLPL 19

RESULT 8

US-08-475-891A-2

Sequence 2, Application US/08475891A

Patent No. 5859339

GENERAL INFORMATION:

APPLICANT: Ronald, Pamela C.

APPLICANT: Wang, Guo-Liang

APPLICANT: Song, Wen-Yuang

TITLE OF INVENTION: Procedures and Materials for Confering

TITLE OF INVENTION: Disease Resistance in Plants

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/475,891A

FILING DATE: 06-JUN-1995

CLASSIFICATION: 800

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/373,375
FILING DATE: 17-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 02370-058910US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1023 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..1023
OTHER INFORMATION: /note= "Xa21 Xanthomonas spp.
OTHER INFORMATION: disease resistance polypeptide RRK-F
OTHER INFORMATION: from rice (Oryza sativa)"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1010
OTHER INFORMATION: /note= "Xaa = Leu when position
OTHER INFORMATION: 5471 of RRK-F = G or Phe when position
OTHER INFORMATION: 5471 of RRK-F = C"
08-567-891A-2
Query Match 6.7%; Score 8; DB 2; Length 1023;
Best Local Similarity 100.0%; Pred. No. 13;
atches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
5 ISSLLLLL 12
10 ISSLLLLL 17

JLT 9
08-567-375-2
Sequence 2, Application US/08567375
Patent No. 5952485
GENERAL INFORMATION:
APPLICANT: Ronald, Pamela C.
APPLICANT: Wang, Guo-Liang
APPLICANT: Song, Wen-Yuang
APPLICANT: Szabo, Veronique
TITLE OF INVENTION: Procedures and Materials for Conferring
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/567,375
FILING DATE: 04-DEC-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/004,645
FILING DATE: 29-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/475,891
FILING DATE: 07-JUN-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/373,375
FILING DATE: 17-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 023070-038930
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1023 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..1023
OTHER INFORMATION: /note= "Xa21 Xanthomonas spp. disease
OTHER INFORMATION: resistance polypeptide RRK-F from rice
OTHER INFORMATION: (Oryza sativa)"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1010
OTHER INFORMATION: /products= "OTHER"
OTHER INFORMATION: /note= "Xaa = Leu when position 5471 of
OTHER INFORMATION: RRK-F = G or Phe when position 5471 of
OTHER INFORMATION: RRK-F = C"
US-08-567-375-2
Query Match 6.7%; Score 8; DB 2; Length 1023;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 5 ISSLLLLL 12
Db 10 ISSLLLLL 17

RESULT 10
US-08-567-680A-2
Sequence 2, Application US/08587680A
Patent No. 5977434
GENERAL INFORMATION:
APPLICANT: Ronald, Pamela C.
APPLICANT: Wang, Guo-Liang
APPLICANT: Song, Wen-Yuang
APPLICANT: Szabo, Veronique
TITLE OF INVENTION: Procedures and Materials for Conferring
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/587,680A
FILING DATE: 17-JAN-1996
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/373,375
FILING DATE: 17-JAN-1995
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/475,891
 FILING DATE: 07-JUN-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/004,645
 FILING DATE: 29-SEP-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/567,375
 FILING DATE: 04-DEC-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Bastian, Kevin L.
 REGISTRATION NUMBER: 34,774
 REFERENCE/DOCKET NUMBER: 023070-058940US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1023 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FEATURE:
 NAME/KEY: Protein
 LOCATION: 1..1023
 OTHER INFORMATION: /note= "Xa21 Xanthomonas spp. disease
 OTHER INFORMATION: resistance polypeptide RRK-F from rice
 OTHER INFORMATION: (Oryza sativa)"
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 1010
 OTHER INFORMATION: /note= "Xaa = Leu when position 5471 of
 OTHER INFORMATION: RRK-F = G or Phe when position 5471 of
 OTHER INFORMATION: RRK-F = C"
 -08-587-680A-2

Query Match 6.7%; Score 8; DB 2; Length 1023;
 Best Local Similarity 100.0%; Pred. No. 13;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

5 ISSLLLLL 12
 10 ISSLLLLL 17

SULT 11
 -08-090-036-1
 Sequence 1, Application US/08090036
 Patent No. 5474922
 GENERAL INFORMATION:
 APPLICANT: Dotreich, Kurt
 APPLICANT: Dalboge, Henrik
 APPLICANT: Mikkelsen, Jan M.
 APPLICANT: Mischler, Marcel
 APPLICANT: Christensen, Flemming M.
 TITLE OF INVENTION: Beta-1,4-GALACTANASE AND A DNA SEQUENCE
 NUMBER OF SEQUENCES: 11
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: No. 5474922o No. 5474922disk of No. 5474922th America, Inc.
 STREET: 405 Lexington Avenue, 62nd Floor
 CITY: New York
 STATE: New York
 COUNTRY: United States of America
 ZIP: 10174-6201
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/090,036
 FILING DATE: 15-JUL-1993
 CLASSIFICATION: 435

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/DK92/00037
 FILING DATE: 06-FEB-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: BE 91610007.6
 FILING DATE: 06-FEB-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Lowrey Dr., Karen A.
 REGISTRATION NUMBER: 31,274
 REFERENCE/DOCKET NUMBER: 3564.204-US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-867-0123
 TELEFAX: 212-867-0298
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 31 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: Aspergillus aculeatus
 STRAIN: CBS 101.43
 US-08-090-036-1

Query Match 5.9%; Score 7; DB 1; Length 31;
 Best Local Similarity 100.0%; Pred. No. 5.1;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 ISSLLLL 11
 DB 9 ISSLLLL 15

RESULT 12
 US-09-390-134B-34
 ; Sequence 34, Application US/09390134B
 ; Patent No. 6518399
 ; GENERAL INFORMATION:
 ; APPLICANT: BARNES, ASHLEY A.
 ; APPLICANT: WISE, ALAN
 ; APPLICANT: MARSHALL, FIONA H.
 ; APPLICANT: FRASER, NEIL J.
 ; APPLICANT: WHITE, JULIE H. M.
 ; APPLICANT: FOORD, STEVEN M.
 ; TITLE OF INVENTION: NOVEL RECEPTOR
 ; FILE REFERENCE: PG3558US2
 ; CURRENT APPLICATION NUMBER: US/09/390,134B
 ; CURRENT FILING DATE: 1999-09-03
 ; PRIOR APPLICATION NUMBER: GB9819420.2
 ; PRIOR FILING DATE: 1998-09-07
 ; NUMBER OF SEQ ID NOS: 55
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 34
 ; LENGTH: 38
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; ORGAN: 390-134B-34

Query Match 5.9%; Score 7; DB 4; Length 38;
 Best Local Similarity 100.0%; Pred. No. 6.1;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LLLLLPL 14
 DB 25 LLLLLPL 31

RESULT 13
 US-09-227-357-212
 ; Sequence 212, Application US/09227357

```

; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 212
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (54)
; OTHER INFORMATION: Xaa equals stop translation
US-09-227-357-212

Query Match          5.9%; Score 7; DB 4; Length 54;
Best Local Similarity 100.0%; Pred.No. 8.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 LLLLLPL 14
        |||||
Db       9 LLLLLPL 15

RESULT 14
US-08-434-705B-6
; Sequence 6, Application US/08434705B
; Patent No. 5798258
; GENERAL INFORMATION:
; APPLICANT: Douglass Ph.D., James
; TITLE OF INVENTION: CART PROTEIN AND DNA ENCODING THEREFOR
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dennis K. Shelton
; STREET: 1420 Fifth Avenue, Suite 2800
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/434,705B
; FILING DATE: May 4, 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Shelton, Dennis K.
; REGISTRATION NUMBER: 26,997
; REFERENCE/DOCKET NUMBER: OHSU18446
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 682-8100
; TELEFAX: (206) 224-0779
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 116 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-434-705B-6

Query Match          5.9%; Score 7; DB 1; Length 116;
Best Local Similarity 100.0%; Pred.No. 17;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 LLLLLPL 14
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Db       16 LLLLLPL 22

RESULT 15
US-09-086-201-6
; Sequence 6, Application US/09086201

```

Thu Feb 19 08:38:56 2004

Patent No. 5969103
GENERAL INFORMATION:
APPLICANT: Douglas Ph.D., James
TITLE OF INVENTION: CART PROTEIN AND DNA ENCODING THEREFOR
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dennis K. Shelton
STREET: 1420 Fifth Avenue, Suite 2800
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/086,201
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/434,705
FILING DATE: May 4, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Shelton, Dennis K.
REGISTRATION NUMBER: 26,997
REFERENCE/DOCKET NUMBER: OHSU18446
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 682-8100
TELEFAX: (206) 224-0779
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
-09-086-201-6
Query Match 5.9%; Score 7; DB 2; Length 116;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
8 LLLLLL 14
16 LLLLLL 22
Arch completed: February 18, 2004, 15:45:16
Time: 30 secs

PRIOR APPLICATION NUMBER: 60/065186	PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311	PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770	PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945	PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910	PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322	PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600	PRIOR FILING DATE: 1998-05-07
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PRIOR APPLICATION NUMBER: 60/087759	PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087827	PRIOR FILING DATE: 1998-06-02
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PRIOR APPLICATION NUMBER: 60/088025	PRIOR FILING DATE: 1998-06-04
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PRIOR APPLICATION NUMBER: 60/091360
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091478
PRIOR FILING DATE: 1998-07-02
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PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Very March 100.0%; Score 119; DB 9; Length 119;
1st Local Similarity 100.0%; Pred. No. 3.5e-101; Indels 0; Gaps 0;
atches 119; Conservative 0; Mismatches 0;

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ILT 2

9-989-723-165
Sequence 165, Application US/09989723
tent No. US20020072092AI

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Deanoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE REFERENCE: P273P1652
CURRENT APPLICATION NUMBER: US/09/989, 723
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
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PRIOR FILING DATE: 1998-07-01
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PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 119; DB 9; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.5e-101;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKVLISLLILLPLMLMSVSSINPGVARGHRRDQASRRWLQEGGQCECKDWFLRAP 60
DB 1 MKVLISLLILLPLMLMSVSSINPGVARGHRRDQASRRWLQEGGQCECKDWFLRAP 60
QY 61 RRKPTVSGLPKKQPCDHFKNVKKTRHQRHRRKPKHSHRACQOFLKQQLRSFALPL 119
DB 61 RRKPTVSGLPKKQPCDHFKNVKKTRHQRHRRKPKHSHRACQOFLKQQLRSFALPL 119

RESULT 3
US-09-989-279-165
; Sequence 165, Application US/09989279
; Patent No. US20020072496A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C56
; CURRENT APPLICATION NUMBER: US/09/989,279
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24

[illegible]

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PRIOR FILING DATE: 1998-07-02
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PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

very Match 100.0%; Score 119; DB 9; Length 119;
est Local Similarity 100.0%; Pred. No. 3.5e-101;
atches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MKVLISLLLLPLMLMSVSSSLNPGVARGHRRDGGASRRWLQEGGQCECKDWFLRAP 60
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61 RKFTVSGLPKQCPCHDFKGNVKKTRHQHRRKPNKHSRACQCFKQQLRSFALPL 119
61 RKFTVSGLPKQCPCHDFKGNVKKTRHQHRRKPNKHSRACQCFKQQLRSFALPL 119

ULT 4
09-989-727-165
sequence 165, Application US/09989727
Patent No. US20020072497A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertitsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: F2730PIC65
CURRENT APPLICATION NUMBER: US/09/989,727
CURRENT FILING DATE: 2001-11-19
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PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
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PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910

PRIOR FILING DATE: 1998-03-20
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PRIOR APPLICATION NUMBER: 60/090695
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090696
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090862
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/090863
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091360
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091478
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091544
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091625

PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 119; DB 9; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.5e-101;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MKVLSSLLLLPLMLSMVSSSLNPGVARGHRDGGQASRRWLQGGQCECKDWFLRAP 60
Db 1 MKVLSSLLLLPLMLSMVSSSLNPGVARGHRDGGQASRRWLQGGQCECKDWFLRAP 60
Oy 61 RRKFTVSGLPKKQCPDHFHKGNVKTRHQRHRRKPNKHSRACQQLKQCOLRSPALPL 119
Db 61 RRKFTVSGLPKKQCPDHFHKGNVKTRHQRHRRKPNKHSRACQQLKQCOLRSPALPL 119

RESULT 5
US-09-989-731-165
; Sequence 165, Application US/09989731
; Patent No. US20020103125A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Baton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C70
; CURRENT APPLICATION NUMBER: US/09/989,731
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28

R/R APPLICATION NUMBER: 60/091978
R/R FILING DATE: 1998-07-07
R/R APPLICATION NUMBER: 60/091982
R/R FILING DATE: 1998-07-07
R/R APPLICATION NUMBER: 60/092182
R/R FILING DATE: 1998-07-09
ery March 100.0%; Score 119; DB 10; Length 119;
st Local Similarity 100.0%; Pred. No. 3.5e-10; Indels 0; Gaps 0;
tches 119; Conservative 0; Mismatches 0;
1 MKVLISLLLLPLMLMSVSSSLNPGVARGHRRDQASRWLQGGQCECKDWFRLAP 60
1 MKVLISLLLLPLMLMSVSSSLNPGVARGHRRDQASRWLQGGQCECKDWFRLAP 60
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61 RRKFTVSGLPKQCPDHFKNVKKTRHQRHRRKPNKHSRACQFLKCCQLRSFALPL 119
LT 6
9-989-732-165
quence 165, Application US/09989732
tent No. US20020123463A1
NERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavini, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C57
URRANT APPLICATION NUMBER: US/09/989,732
URRANT FILING DATE: 2001-11-19
R/R APPLICATION NUMBER: 60/049787
R/R FILING DATE: 1997-06-16
R/R APPLICATION NUMBER: 60/062250
R/R FILING DATE: 1997-10-17
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R/R FILING DATE: 1997-11-12
R/R APPLICATION NUMBER: 60/065311
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R/R APPLICATION NUMBER: 60/066770
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R/R APPLICATION NUMBER: 60/075945
R/R FILING DATE: 1998-02-25
R/R APPLICATION NUMBER: 60/078910
R/R FILING DATE: 1998-03-20
R/R APPLICATION NUMBER: 60/083322
R/R FILING DATE: 1998-04-28
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; PRIOR FILING DATE: 1998-06-17
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; PRIOR FILING DATE: 1998-06-17

PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089907
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089908
PRIOR FILING DATE: 1998-06-18
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PRIOR APPLICATION NUMBER: 60/091544
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982

PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09
Query Match 100.0%; Score 119; DB 10; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.5e-101; Indels 0; Gaps 0;
Matches 119; Conservative 0; Mismatches 0;
Qy 1 MKVLISLLLLPLMLMSVSSSLNPGVARGHRDGGQASRRWLQEGGQCECKDFLEAP 60
Db 1 MKVLISLLLLPLMLMSVSSSLNPGVARGHRDGGQASRRWLQEGGQCECKDFLEAP 60
Qy 61 RRKFTVSGLPKKQCECDHFKGNVKKTRHQRHRRKPNKHSRACQQLKCCQLRSFALPL 119
Db 61 RRKFTVSGLPKKQCECDHFKGNVKKTRHQRHRRKPNKHSRACQQLKCCQLRSFALPL 119
RESULT 7
US-09-991-073-165
Sequence 165, Application US/09991073
Patent No. US20020127576A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavini, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas P.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C15
CURRENT APPLICATION NUMBER: US/09/991,073
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
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PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02

[illegible]

Very Match 100.0%; Score 119; DB 10; Length 119;
1st Local Similarity 100.0%; Pred. No. 3.5e-101; Indels 0; Gaps 0;
atches 119; Conservative 0; Mismatches 0;
1 MKVLISLLLLPLMLMSVSSSLNPGVARGHRDRGQASRWTLQEGGQCECKDWFLRAP 60
1 MKVLISLLLLPLMLMSVSSSLNPGVARGHRDRGQASRWTLQEGGQCECKDWFLRAP 60
61 RKKEWTVSGLPKKQPCDHPKGNVKKTRHQRHKKPNKHSRACQQLKOCQRLSFPALPL 119
61 RKKEWTVSGLPKKQPCDHPKGNVKKTRHQRHKKPNKHSRACQQLKOCQRLSFPALPL 119

JLT 8

09-990-442-165
sequence 165; Application US/099930442
agent No. US20020122252A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnovers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PIC8
CURRENT APPLICATION NUMBER: US/09/990,442
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
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PRIOR FILING DATE: 1997-11-13
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PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087609
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087759

PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087827
PRIOR FILING DATE: 1998-06-03
PRIOR APPLICATION NUMBER: 60/088021
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088025
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PRIOR FILING DATE: 1998-06-18

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R10R FILING DATE: 1998-07-02
R10R APPLICATION NUMBER: 60/091978
R10R FILING DATE: 1998-07-07
R10R APPLICATION NUMBER: 60/091982
R10R FILING DATE: 1998-07-07
R10R APPLICATION NUMBER: 60/092182
R10R FILING DATE: 1998-07-09

Very Match 100.0%; Score 119; DB 10; Length 119;
1st Local Similarity 100.0%; Pred. No. 3.5e-101;

Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 9

US-09-991-163-165
; Sequence 165, Application US/09991163
; Patent No. US20020132253A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730PIC17
; CURRENT APPLICATION NUMBER: US/09/991,163
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 119; DB 10; Length 119;
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LT 10
9-993-604-165

Quence 165, Application US/09993604

test No. US20020137075A1

NERAL INFORMATION:

PPPLICANT: Ashkenazi, Avi J.

PPPLICANT: Baker, Kevin P.

PPPLICANT: Botstein, David

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PPPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

TITLE OF INVENTION: Acids Encoding the Same

TITLE REFERENCE: P2730P1C25

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PRIOR APPLICATION NUMBER: 60/089952
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Prior Application Number: 60/090246
Prior Filing Date: 1998-06-22
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Prior Filing Date: 1998-06-24
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Prior Filing Date: 1998-06-24
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Prior Filing Date: 1998-07-02
Prior Application Number: 60/091626
Prior Filing Date: 1998-07-02
Prior Application Number: 60/091633
Prior Filing Date: 1998-07-02
Prior Application Number: 60/091978
Prior Filing Date: 1998-07-07
Prior Application Number: 60/091982
Prior Filing Date: 1998-07-07
Prior Application Number: 60/092182
Prior Filing Date: 1998-07-09

Query Match 100.0%; Score 119; DB 10; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.5e-101;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; Patent No. US20020137890A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deenoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
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; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
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; CURRENT FILING DATE: 2001-11-14
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 PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 119; DB 10; Length 119;
 Best Local Similarity 100.0%; Pred. No. 3.5e-101;
 Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MKVLISLLLLPLMLMSVSSSLNPGVARGHRDRGQASRRWLQGGQCECKDWFLRAP 60
 Db 1 MKVLISLLLLPLMLMSVSSSLNPGVARGHRDRGQASRRWLQGGQCECKDWFLRAP 60
 Qy 61 RRKFTVSGLPKKQCFCDHFKGNVKTTRHQRHHRKPKHRSACQOFLKQCOLRSFALPL 119
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R10R FILING DATE: 1998-07-02
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R10R FILING DATE: 1998-07-07
R10R APPLICATION NUMBER: 60/091982
R10R FILING DATE: 1998-07-07
R10R APPLICATION NUMBER: 60/092182
R10R FILING DATE: 1998-07-09

very Match 100.0%; Score 119; DB 10; Length 119;
est Local Similarity 100.0%; Pred. No. 3.5e-101;
atches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 MKVLISLLLLPLMLSMVSSSLNPGVARGHRRDGGASRRWLQEGGQCECKQWFLRAP 60
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61 RRKFMTVSGLPKQCPCDHFHGNKVKTRHQRHHRKPNKHSRAQQQFLKQCQLRSFALPL 119
61 RRKFMTVSGLPKQCPCDHFHGNKVKTRHQRHHRKPNKHSRAQQQFLKQCQLRSFALPL 119

ULT 13

US-09-992-598-165
; Sequence 165, Application US/09992598
; Patent No. US20020160384A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730PIC20
; CURRENT APPLICATION NUMBER: US/09/992,598
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
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PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 119; DB 10; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.5e-101; Indels 0; Gaps 0;
Matches 119; Conservative 0; Mismatches 0;

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Db 1 MKVLISLLLLPLMLSMVSSSLNPGVARGHRRDQGASRWLQEGGQCECKDWFTRAP 60
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Db 61 RRFMTVSGLPKQCPDHFKNYKTHORHHRKPNKHSACQFLKQCOLRSFALPL 119

RESULT 14
US-09-989-293A-165
; Sequence 165, Application US/09989293A
; Patent No. US20020177164A1

INTERNAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
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APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoli, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C66
CURRENT APPLICATION NUMBER: US/09/989,293A
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/0493787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
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PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 119; DB 10; Length 119;
Best Local Similarity 100.0%; Pred.No.3.5e-101;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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SUIT 15
-09-989-735-165
Sequence 165, Application US/09989735
Publication No. US20020193299A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
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APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC61
CURRENT APPLICATION NUMBER: US/09/989,735
CURRENT FILING DATE: 2001-11-19
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R10R APPLICATION NUMBER: 60/090535
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R10R FILING DATE: 1998-06-24
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R10R APPLICATION NUMBER: 60/091633
R10R FILING DATE: 1998-07-02
R10R APPLICATION NUMBER: 60/091978
R10R FILING DATE: 1998-07-07
R10R APPLICATION NUMBER: 60/091982
R10R FILING DATE: 1998-07-07
R10R APPLICATION NUMBER: 60/092182
R10R FILING DATE: 1998-07-09

Query Match 100.0%; Score 119; DB 10; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.5e-101; Indels 0; Gaps 0;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 MKVLISLILLLPLMLMSVSSLNPGVARGHRDRGQASRRWLQGGQCECKDWFLRAP 60
Qy 61 RRFMTVSGLPKKQPCDHFKNVKTTHQHRHKNKHSBACQFLKQCOLRSFALPL 119
Db 61 RRFMTVSGLPKKQPCDHFKNVKTTHQHRHKNKHSBACQFLKQCOLRSFALPL 119

Search completed: February 18, 2004, 15:46:06
Job time : 35 secs

GenCore version 5.1.1.6
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rotein - protein search, using sw model

on: February 18, 2004, 15:34:55 ; Search time 21 Seconds
(without alignments)
544.956 Million cell updates/sec

e: US-09-786-260-1
ect score: 119
ence: 1 MKVLISLLLLPLMLMSNV.....SPACQFLKQQLRSPALPL 119

ing table: OLIGO
Gapop 60.0 , Gapext 60.0

ched: 283308 seqs, 96168682 residues

i size: 0

l number of hits satisfying chosen parameters: 283308

mm DB seq length: 0
mm DB seq length: 2000000000

rocessing: Listing first 45 summaries

base:

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

hit No.	Score	Query Match	Length	ID	Description
1	8	6.7	86	2 C71549	hypothetical prote
2	8	6.7	109	2 B70037	hypothetical prote
3	8	6.7	360	2 JX0281	alpha-2-macroglobu
4	8	6.7	449	2 D87284	sensory box histid
5	8	6.7	453	2 A53735	exoenzyme S - Pseu
6	8	6.7	594	2 B90586	transport protein
7	8	6.7	1305	2 AD0428	probable exported
8	7	5.9	42	2 PH1333	Ig heavy chain bu
9	7	5.9	52	2 AF0293	hypothetical prote
10	7	5.9	97	4 S26485	cytochrome P450 21
11	7	5.9	107	2 S39207	hypothetical prote
12	7	5.9	117	2 S31130	hypothetical prote
13	7	5.9	157	2 B69476	inosine monophosph
14	7	5.9	174	1 TVVP44	small T antigen -
15	7	5.9	187	2 A86363	hypothetical prote
16	7	5.9	189	2 G96682	Flp19.3 (imported
17	7	5.9	202	2 A75261	conserved hypothet
18	7	5.9	203	2 C64038	hypothetical prote
19	7	5.9	205	2 S37804	hypothetical prote
20	7	5.9	209	2 A54984	ELP-1 protein prec
21	7	5.9	213	2 JE0322	eprlin-A2 - human
22	7	5.9	217	2 D96658	hypothetical prote
23	7	5.9	220	2 S43291	flr3/FUK2 ligand (
24	7	5.9	220	2 I58343	flr3 ligand isofor
25	7	5.9	227	2 C64355	conserved hypothet
26	7	5.9	231	2 A49265	flr3/flk-2 ligand
27	7	5.9	247	2 G83382	conserved hypothet
28	7	5.9	249	2 T35589	probable secreted
29	7	5.9	250	2 D75317	hypothetical prote

hypothetical prote
interleukin 15 rec
TNF6.7 protein - A
probable transport
probable transport
probable membrane
gene MAC25 protein
hypothetical prote
prostaglandin-simu
conserved hypothet
probable polynucle
trypsin homolog -
ABC transporter su
probable peroxidas
beta-N-acetyl-D-gl
hrpv protein - Pse

30 7 5.9 262 2 G90493
31 7 5.9 263 2 S57346
32 7 5.9 263 2 H86147
33 7 5.9 264 2 G90884
34 7 5.9 264 2 H85733
35 7 5.9 264 2 F64896
36 7 5.9 277 2 I52825
37 7 5.9 280 2 F67668
38 7 5.9 282 2 S50031
39 7 5.9 294 2 B71256
40 7 5.9 295 2 B83587
41 7 5.9 303 2 T13598
42 7 5.9 319 2 G82694
43 7 5.9 329 2 F84640
44 7 5.9 332 2 G83270
45 7 5.9 333 2 S61849

RESULT 1
C71549
hypothetical protein C7164 - Chlamydia trachomatis (serotype D, strain UW3/Cx)
C/Species: Chlamydia trachomatis
C/Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 08-Oct-1999
C/Accession: C71549
R/Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell, Science 282, 754-759, 1998
A/Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trac
A/Reference number: A71570; MUID:99000809; PMID:9784136
A/Accession: C71549
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-86 <ARN>
A/Cross-references: GB:AE001290; GB:AE001273; NID:G3328560; PIDN:AAC67755.1; PID:G332856
A/Experimental source: serotype D, strain UW-3/Cx
C/Genetics:
A/Gene: C7164

Query Match 6.7%; Score 8; DB 2; Length 86;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 ISLILLLL 12
Db 46 ISLILLLL 53

RESULT 2
B70037
hypothetical protein yvfA - Bacillus subtilis
C/Species: Bacillus subtilis
C/Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 15-Oct-1999
C/Accession: B70037
R/Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch C.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Eyring, J.; Fabet, C.; Ferrari, E. Nature 390, 249-256, 1997
A/Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A/Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel Y, M.; Ogawa, K.; Ogihara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, A/Authors: Schleitch, S.; Schreter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seron ikeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpetra, P.; Tognoni, A.; Tostato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, f A/Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A/Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A/Reference number: A69580; MUID:98044033; PMID:9384377
A/Accession: B70037
A/Status: preliminary; nucleic acid sequence not shown; translation not shown

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Cleavage type: DNA
residues: 1-109 <KUN>
cross-references: GB:Z99121; GB:AL009126; NID:G2635827; PIDN:CAB15432.1; PID:el186115;
experimental source: strain 168
enetics:
ene: yvfa

Query Match 6.7%; Score 8; DB 2; Length 109;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

4 LLSLLLL 11
269 LLSLLLL 276

RESULT 5
A53735
exoenzyme S - Pseudomonas aeruginosa
NAlternate names: ADP-ribosyltransferase (EC 2.4.2.-); exoS
CSpecies: Pseudomonas aeruginosa
CDate: 07-Oct-1994 #sequence_revision 06-Oct-2000 #text_change 31-Dec-2000
CAccession: A53735; B83166
R.Kulich, S.M.; Yahr, T.L.; Mende-Mueller, L.M.; Barbieri, J.T.; Frank, D.W.
J. Biol. Chem. 269, 10431-10437, 1994
A>Title: Cloning the structural gene for the 49-kDa form of exoenzyme S (exoS) from Pse
AReference number: A53735; MUID:94193734; PMID:8144626
AAccession: A53735
AStatus: preliminary
AMolecule type: DNA
AResidues: 1-453 <KUL>
A.Cross-references: GB:L27629; NID:G639898; PIDN:AAA66491.1; PID:g450297
R.Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; B
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A>Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic path
AReference number: A82950; MUID:20437337; PMID:10984043
AAccession: B83166
AStatus: preliminary
AMolecule type: DNA
AResidues: 1-453 <STO>
A.Cross-references: GB:AE004801; GB:AE004091; NID:G9950011; PIDN:AAG07228.1; GSPDB:GN00
AExperimental source: strain PA01
CGenetics:
CKeywords: glycosyltransferase; pentosyltransferase

Query Match 6.7%; Score 8; DB 2; Length 453;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

23 SLNPGVAR 30
345 SLNPGVAR 352

RESULT 6
B90586
transport protein sgat [imported] - Mycoplasma pulmonis (strain UAB CTIP)
CSpecies: Mycoplasma pulmonis
CDate: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001
CAccession: B90586
R.Chanbaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galissen, F.; Moszer, I
Nucleic Acids Res. 29, 2145-2153, 2001
A>Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pul
AReference number: A99512; MUID:21267165; PMID:11353084
AAccession: B90586
AStatus: preliminary
AMolecule type: DNA
AResidues: 1-594 <KUR>
A.Cross-references: GB:AL445566; PID:g14090009; PIDN:CAC13767.1; GSPDB:GN00153
AExperimental source: strain UAB CTIP
CGenetics:
AGene: MYPV 5940
AGenetic code: SGC3

Query Match 6.7%; Score 8; DB 2; Length 594;
Best Local Similarity 100.0%; Pred. No. 7.7;

ULT 3
ha-2-macroglobulin receptor-associated protein precursor - mouse
lternate names: heparin-binding protein-44
lternate names: Mus musculus (house mouse)
ate: 19-May-1994 #sequence_revision 19-May-1994 #text_change 20-Jun-2000
ccession: JX0281; JX0126
akamoto, M.; Ozawa, M.; Jacinto, S.D.; Furukawa, T.; Natori, Y.; Shirahama, H.; Yonez
Biochem. 114, 344-349, 1993
ltitle: Mouse heparin binding protein-44 (HBP-44) associates with brushin, a high-molec
eference number: JX0281; MUID:94110255; PMID:8282724
ccession: JX0281
lolecule type: mRNA
esidues: 1-360 <NAK>
ross-references: GB:S67967; NID:G460891; PIDN:AA0668.1; PID:g460892
urukawa, T.; Ozawa, M.; Huang, R.P.; Muramatsu, T.
Biochem. 108, 297-302, 1990
ltitle: A heparin binding protein whose expression increases during differentiation of
eference number: JX0126; MUID:91035363; PMID:2229028
ccession: JX0126
lolecule type: mRNA
esidues: 2-360 <FUR>
ross-references: GB:D00622; NID:G220433; PIDN:BAA0500.1; PID:g220434
ywords: chondroitin sulfate proteoglycan; Glycoprotein; heparin binding
-37/Domain: signal sequence #status predicted <SIG>
8-360/Product: alpha-2-macroglobulin receptor-associated protein #status predicted <M
3.164/Binding site: chondroitin sulfate (Ser) (covalent) #status predicted
71/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 6.7%; Score 8; DB 2; Length 360;
Best Local Similarity 100.0%; Pred. No. 5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

9 LLLPLML 16
19 LLLPLML 26

ULT 4
284
sory box histidine kinase [imported] - Caulobacter crescentus
pecies: Caulobacter crescentus
ate: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
ccession: D87284
ierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Shapiro, J.C.; Fraser, C.M.
c. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
ltitle: Complete Genome Sequence of Caulobacter crescentus.
eference number: A87249; MUID:21173698; PMID:11259647
ccession: D87284
tatus: preliminary
lolecule type: DNA
esidues: 1-449 <STO>
ross-references: GB:AE005673; NID:G13421422; PIDN:AAK22272.1; GSPDB:GN00148
enetics:
ene: CC0285
```


tches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

3 VLISLL 10
|||||
231 VLISLL 238

LT 7
28
able exported protein YPO3523 [imported] - Yersinia pestis (strain CO92)
ecies: Yersinia pestis
te: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001
cession: AD0428
khill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
re 413, 523-527, 2001
tle: Genome sequence of Yersinia pestis, the causative agent of plague.
ference number: AB0001; MUID:21470413; PMID:11586360
cession: AD0428
atus: preliminary
lecul type: DNA
sidues: 1-1305 <KUR>
oss-references: GB:AL590842; PIDN:CA92752.1; PID:G15981447; GSPDB:GN00175
ne: YPO3523
perfamily: ytfN protein

ery Match 6.7%; Score 8; DB 2; Length 1305;
st Local Similarity 100.0%; Pred. No. 15;
tches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

3 VLISLL 10
|||||
299 VLISLL 306

LT 8
33
eavy chain DJ region (clone C238-133) - human (fragment)
ecies: Homo sapiens (man)
te: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
cession: PH1333
seerman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
xp. Med. 176, 1577-1581, 1992
tle: Predominance of fetal type DJH joining in young children with B precursor lymph
ference number: PH1302; MUID:93094761; PMID:1460419
cession: PH1333
lecul type: DNA
sidues: 1-22 <WAS>
ywords: heterotrimer; immunoglobulin

ery Match 5.9%; Score 7; DB 2; Length 22;
st Local Similarity 100.0%; Pred. No. 4.5;
tches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

7 SLLLLP 13
|||||
8 SLLLLP 14

LT 9
93
thetical protein YPO2405 [imported] - Yersinia pestis (strain CO92)
ecies: Yersinia pestis
te: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
cession: AF0293
khill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
re 413, 523-527, 2001
tle: Genome sequence of Yersinia pestis, the causative agent of plague.
ference number: AB0001; MUID:21470413; PMID:11586360

A:Accession: AF0293
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-52 <KUR>
A:Cross-references: GB:AL590842; PIDN:CA92752.1; PID:G15980400; GSPDB:GN00175
C:Genetics:
A:Gene: YPO2405

Query Match 5.9%; Score 7; DB 2; Length 52;
Best Local Similarity 100.0%; Pred. No. 9.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 SLLLLP 13
|||||
Db 36 SLLLLP 42

RESULT 10
S26485
cytochrome P450 21A/B mutant fusion protein - human
N:Alternate names: steroid 21-monooxygenase
C:Species: Homo sapiens (man)
C>Date: 06-Jan-1995 #sequence_revision 17-Aug-1995 #text_change 15-Feb-1996
C:Accession: S26485; S29672
R:Helmsberg, A.; Kofler, R.
submitted to the EMBL Data Library, March 1991
A:Reference number: S26484
A:Accession: S26485
A:Molecule type: DNA
A:Residues: 1-97 <HEL>
A:Cross-references: EMBL:X58901
A:Experimental source: leukocyte clone AGS 8-23
A>Note: an unequal cross-over mutation of the CYP21P pseudogene and CYP21 gene in a cong
A:Accession: S29672
A:Molecule type: DNA
A:Residues: 1-97 <HE2>
A:Cross-references: EMBL:X58908
C:Genetics:
A:Gene: CYP21P/CYP21
A:Map position: 6p21.3
A:Introns: 68/1
C:Keywords: fusion protein

Query Match 5.9%; Score 7; DB 4; Length 97;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LLLLLP 14
|||||
Db 6 LLLLLP 12

RESULT 11
S39207
hypothetical protein 2 - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 19-May-2000
C:Accession: I61221; S39207
R:Courty, Y.; Rosinski-Chupin, I.; Rougeon, F.
J. Biol. Chem. 269, 520-527, 1994
A:Title: A new proline-rich protein precursor expressed in the salivary glands of the ra
A:Reference number: A53118; MUID:94103265; PMID:8276845
A:Accession: I61221
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-107 <COU>
A:Cross-references: EMBL:X74229; NID:9433616; PIDN:CAA52301.1; PID:G433618
A>Note: submitted to the EMBL Data Library, July 1993
C:Comment: This is translated in an alternate reading frame of the proline-rich protein

Query Match 5.9%; Score 7; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

JUT 12
130
schematic protein F5982.10 - Caenorhabditis elegans
Species: Caenorhabditis elegans
Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 04-Mar-2000
Accession: S31130
Winston, J.; Du, Z.; Thomas, K.; Wilson, R.; Hillier, L.; Staden, R.; Halloran, N.; Gilman, T.; Ainscough, R.; Waterston, R.
Submitted to the EMBL Data Library, November 1991
Description: The C. elegans sequencing project: A beginning.
Reference number: S31122
Accession: S31130
Status: preliminary
Molecule type: DNA
Residues: 1-117 <SUL>
Cross-references: EMBL:Z11505; NID:G6718; PID:G6727
Enetics:
ntrons: 21/2; 74/1
uperfamily: Caenorhabditis elegans hypothetical protein F5982.10

Query Match 5.9%; Score 7; DB 2; Length 117;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 ISSLLLLL 11
DB 8 ISSLLLLL 14

ULT 13
476
sine monophosphate cyclohydrolase homolog - Archaeoglobus fulgidus
Species: Archaeoglobus fulgidus
Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
Accession: B69476
Lank, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
Odek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
ure 390, 364-370, 1997
Authors: Overbeek, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
th, H.O.; Woese, C.R.; Venter, J.C.
Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaea
Reference number: A69250; MUID:98049343; PMID:9389475
Accession: B69476
Status: preliminary; nucleic acid sequence not shown; translation not shown
Molecule type: DNA
Residues: 1-157 <KLE>
Cross-references: GB:AE000378; GB:AE000782; NID:G2689301; PIDN:AAB89440.1; PID:G264873

Query Match 5.9%; Score 7; DB 2; Length 157;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKVLISS 7
DB 1 MKVLISS 7

ULT 14
784
ll T antigen - rhesus polyomavirus
Species: Polyomavirus maccacae 1 (rhesus polyomavirus, SV40)
Date: 30-Nov-1980 #sequence_revision 30-Nov-1980 #text_change 22-Oct-1999
Accession: C03631; C36763; A03618
teddy, V.B.; Thimmappaya, B.; Dhar, R.; Subramanian, K.N.; Zain, B.S.; Pan, J.; Ghosh,
ence 200, 494-502, 1978
Title: The genome of simian virus 40.

A:Reference number: A03631; MUID:78159686; PMID:205947
A:Accession: C03631
A:Molecule type: DNA
A:Residues: 1-174 <RED>
A:Cross-references: GB:J02400; GB:J02402; GB:J02403; GB:J02406; GB:J02407; GB:J02408; GE
35061
R:Piers, W.; Contreras, R.; Haegeman, G.; Rogiers, R.; van de Voorde, A.; van Heuverswy
Nature 273, 113-120, 1978
A:Title: Complete nucleotide sequence of SV40 DNA.
A:Reference number: A36763; MUID:78156432; PMID:205802
A:Accession: C36763
A:Molecule type: DNA
A:Residues: 1-174 <PIE>
A:Cross-references: GB:V01380; NID:G62000; PIDN:CAA24673.1; PID:G62005
A:Experimental source: strain 776
C:Comment: The initial 82 residues of the large T and small t antigens from SV40 are co
C:Superfamily: small t antigen; dnaJ amino-terminal homology
C:Keywords: acetylated amino end; early protein
F:12-62/Domain: dnaJ amino-terminal homology #status atypical <DNJ>
F:1/Modified site: acetylated amino end (Met) #status experimental

Query Match 5.9%; Score 7; DB 1; Length 174;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 SSLNPGV 28
DB 86 SSLNPGV 92

RESULT 15
A86363
hypothetical protein F19G10.14 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001
C:Accession: A86363
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso
Chen, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K
ansen, N.F.; Hughes, B.; Ruizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziali
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: A86363
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-187 <STO>
A:Cross-references: GB:AE005172; NID:G2462834; PIDN:AAB72169.1; GSPDB:GN00141
C:Genetics:
A:Map position: 1

Query Match 5.9%; Score 7; DB 2; Length 187;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LLLLLLPL 14
DB 6 LLLLLLPL 12

Search completed: February 18, 2004, 15:44:46
Job time : 34 secs

GenCore version 5.1.6
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rotein - protein search, using sw model

on: February 18, 2004, 14:41:55 ; Search time 13 Seconds
(without alignments)
430.475 Million cell updates/sec

e: US-09-786-260-1

ect score: 119

ence: 1 MKVLISLLLLPLMLMSNV.....SRACQFLKQQLRSFALPL 119

ing table: OLIGO

Gapop 60.0 , Gapext 60.0

ched: 127863 seqs, 47026705 residues

(size : 0

1 number of hits satisfying chosen parameters: 127863

mum DB seq length: 0

mum DB seq length: 2000000000

-processing: Listing first 45 summaries

base : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

ult	lc.	Score	Query Match	Length	DB	ID	Description
1	8	7.6	837	1	PHLD_MOUSE	O70362	mus musculus
2	9	7.6	360	1	AMRP_MOUSE	P55302	mus musculus
3	7	5.9	106	1	YKJ0_CAEEL	P34485	caenorhabdi
4	7	5.9	107	1	PRK2_RAT	O84113	rattus norv
5	7	5.9	128	1	PRK2_MOUSE	O96x17	mus musculus
6	7	5.9	129	1	CART_MOUSE	P56388	mus musculus
7	7	5.9	129	1	CART_RAT	P49192	rattus norv
8	7	5.9	145	1	RL2A_TRYBB	O15883	trypanosoma
9	7	5.9	154	1	RNS6_BOVIN	P08904	bos taurus
10	7	5.9	174	1	TASM_SV40	P03081	simian viru
11	7	5.9	202	1	YP37_DHIRA	O92rf5	deinococcus
12	7	5.9	203	1	YGMW_HAEIN	P44272	haemophilus
13	7	5.9	205	1	YK07_YEAST	P36061	saccharomyc
14	7	5.9	209	1	EFA2_MOUSE	P52801	mus musculus
15	7	5.9	211	1	CLDD_MOUSE	O94084	mus musculus
16	7	5.9	213	1	EFA2_HUMAN	O43921	homo sapien
17	7	5.9	227	1	Y443_METJA	O57885	methanococc
18	7	5.9	230	1	SGY1_MOUSE	O98219	mus musculus
19	7	5.9	232	1	FU3L_MOUSE	P43772	mus musculus
20	7	5.9	245	1	CIQC_HUMAN	P02747	homo sapien
21	7	5.9	249	1	YBGO_STRCO	P40179	streptomyce
22	7	5.9	264	1	YDCV_ECOLI	P77505	escherichia
23	7	5.9	281	1	IBP7_MOUSE	O61581	mus musculus
24	7	5.9	282	1	IBP7_HUMAN	O16270	homo sapien
25	7	5.9	329	1	PE18_ARATH	O98k52	arabidopsis
26	7	5.9	332	1	NAGZ_PSEAE	O98k52	arabidopsis
27	7	5.9	339	1	SRG7_CABEL	P54129	pseudomonas
28	7	5.9	350	1	GAN4_ASPAC	P48842	aspergillus
29	7	5.9	364	1	CD33_HUMAN	P20138	homo sapien
30	7	5.9	367	1	DIAC_RAT	O01460	rattus norv
31	7	5.9	372	1	CD14_RABIT	O28680	oryctolagus
32	7	5.9	375	1	CD14_HUMAN	P08571	homo sapien
33	7	5.9	388	1	OFU1_HUMAN	O98488	homo sapien

ALIGNMENTS

RESULT 1

ID	PHLD_MOUSE	STANDARD;	PRT;	837 AA.
AC	O70362;			
DT	30-MAY-2000 (Rel. 39, Created)			
DT	30-MAY-2000 (Rel. 39, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	Phosphatidylinositol-glycan-specific phospholipase D 1 precursor			
DE	(EC 3.1.4.50) (PI-G PLD) (Glycoprotein phospholipase D) (Glycosyl-			
DE	phosphatidylinositol specific phospholipase D).			
GN	GPLD1.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Glucagonoma;			
RX	MEDLINE=98384535; PubMed=9716655;			
RA	LeBoeuf R.C., Caldwell M., Guo Y., Metz C., Davitz M.A., Olson L.K.,			
RA	Deeg M.A.;			
RT	"Mouse glycosylphosphatidylinositol-specific phospholipase D (Gpld1)			
RT	characterization."			
RL	Mamm. Genome 9:710-714 (1998).			
CC	-I- FUNCTION: This protein hydrolyzes the inositol phosphate linkage			
CC	in proteins anchored by phosphatidylinositol glycans (GPI-anchor)			
CC	thus releasing these proteins from the membrane.			
CC	-I- CATALYTIC ACTIVITY: 6-(alpha-D-glucosaminyl)-1-phosphatidyl-1D-			
CC	myo-inositol + H(2)O = 6-(alpha-D-glucosaminyl)-1D-myo-inositol +			
CC	phosphatidate.			
CC	-I- SUBCELLULAR LOCATION: Secreted.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	EMBL; AF050666; AAC77799.1; ..			
DR	MED; MG1:106604; Gpld1			
DR	GO; GO:0008507; P:GPI anchor release; IDA.			
DR	InterPro; IPR01028; Gpdt-Flipase.			
DR	InterPro; IPR000413; Integrin_alpha.			
DR	Pfam; PF01839; FG-GAP; 4.			
DR	SMART; PR00718; PHPLIPASED.			
DR	SMART; SM00191; Int alpha; 5.			
KW	Hydrolase; Glycoprotein; Signal.			
FT	SIGNAL 1 23			
FT	CHAIN 24 837			
FT	BY SIMILARITY			
FT	PROPHATIDYLINOSITOL-GLYCAN-SPECIFIC			
FT	PHOSPHOLIPASE D 1.			
FT	CARBOHYD 94 94			
FT	N-LINKED (GLCNAC. . .) (POTENTIAL).			
FT	CARBOHYD 267 267			
FT	N-LINKED (GLCNAC. . .) (POTENTIAL).			
FT	CARBOHYD 287 287			
FT	N-LINKED (GLCNAC. . .) (POTENTIAL).			
FT	CARBOHYD 303 303			
FT	N-LINKED (GLCNAC. . .) (POTENTIAL).			

P01137 homo sapien
Q912w2 mus musculus
O96009 homo sapien
O06377 mycobacteri
O12976 xenopus lae
P41298 balaenopter
P24975 balaenopter
P03910 bos taurus
Q92258 canis famil
Q8w9m7 dugong dugon
P92484 equus asinu
P48916 felis silve

CARBOHYD 317 317 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CARBOHYD 477 477 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CARBOHYD 496 496 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CARBOHYD 586 586 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CARBOHYD 599 599 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CARBOHYD 655 655 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SEQUENCE 837 AA; 93255 MW; 90007F479556CCCL CRC64;

Query Match 7.6%; Score 9; DB 1; Length 837;

Best Local Similarity 100.0%; Pred. No. 0.86;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

6 SLLILLPL 14
 |||||
 8 SLLILLPL 16

ULT 2

P_MOUSE
 AMRP MOUSE STANDARD; PRT; 360 AA.
 P55302;
 01-OCT-1996 (Rel. 34, Created)
 16-OCT-1996 (Rel. 34, Last sequence update)
 16-OCT-2001 (Rel. 40, Last annotation update)
 Alpha-2-macroglobulin receptor-associated protein precursor
 (Alpha-2-MRAP) (Low density lipoprotein receptor-related protein-
 associated protein 1) (RAP) (Heparin binding protein-44) (HBP-44).
 LRPA1.
 Mus musculus (Mouse).
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 [1]

SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

MEDLINE=94110255; PubMed=8282724;
 Nakamoto M., Ozawa M., Jacinto S.D., Furukawa T., Natori Y.,
 Shirahama H., Yonezawa S., Nakayama T., Muramatsu T.;
 "Mouse heparin binding protein-44 (HBP-44) associates with brushin, a
 high-molecular-weight glycoprotein antigen common to the kidney and
 teratocarcinomas";
 J. Biochem. 114:344-349 (1993).

-1- FUNCTION: INTERACTS WITH THE ALPHA-2-MACROGLOBULIN RECEPTOR AND
 GLYCOPROTEIN 330.
 -1- SUBUNIT: PRESENT ON CELL SURFACE FORMING A COMPLEX WITH THE ALPHA-
 2-MACROGLOBULIN RECEPTOR HEAVY AND LIGHT CHAINS (BY SIMILARITY).
 -1- SUBCELLULAR LOCATION: INTRACELLULAR AND ASSOCIATED WITH CELL
 SURFACE RECEPTORS (BY SIMILARITY).
 -1- SIMILARITY: TO HOMOLOGS IN OTHER MAMMALIAN SPECIES.

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 or send an email to license@isb-sib.ch).

EMBL; S67967; AAC0668.1; -
 PIR; JX0281; JX0281.
 HSP; P30533; 1LRE.
 MGD; MGI:96829; Lrpap1.
 InterPro; IPR000886; ER target.
 PROSITE; PS00014; ER TARGET; 1.
 Signal; Heparin-binding; Glycoprotein; Antigen.
 SIGNAL 1 28 POTENTIAL.
 CHAIN 29 360 ALPHA-2-MACROGLOBULIN RECEPTOR-ASSOCIATED
 PROTEIN.

DOMAIN 240 356 LDL RECEPTOR BINDING (POTENTIAL).
 CARBOHYD 271 271 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SITE 357 360 PREVENT SECRETION FROM ER (POTENTIAL).
 SEQUENCE 360 AA; 42215 MW; 72ED46FA0AC05D51 CRC64;

Query Match 6.7%; Score 8; DB 1; Length 360;

Best Local Similarity 100.0%; Pred. No. 3.7;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 LLLPLML 16
 |||||
 DB 19 LLLPLML 26
 |||||

RESULT 3

YMOJ CAEEL YMOJ CAEEL STANDARD; PRT; 106 AA.
 AC P34485;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Hypothetical protein F59B2.10 in chromosome III.
 GN F59B2.10.

OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 CX NCBI_TaxID=6239;
 RN [1]

SEQUENCE FROM N.A.

RC STRAIN=Bristol N2;
 MEDLINE=94150718; PubMed=7906398;
 RA Wilson R., Alnsough R., Anderson K., Baynes C., Berks M.,
 Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
 Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
 Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
 Johnston D., Jones M., Kershaw J., Kirsten J., Laister N.,
 Lareille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
 Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkeen R.,
 Sims M., Smalton N., Smith A., Smith M., Sonhammer E., Staden R.,
 Sultun J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
 Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,
 Wohlman P.;
 RA "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 elegans";
 RL Nature 368:32-38 (1994).
 RN [2]

RP REVISIONS.

RA Durbin R.;
 RL Submitted (SBP-2001) to the EMBL/GenBank/DBJ databases.
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 or send an email to license@isb-sib.ch).

CC -----
 DR EMBL; Z11505; CAI7587.2; -
 DR WormPep; F59B2.10; CE28835.
 KW Hypothetical protein.
 FT DOMAIN 11 14 POLY-LEU.
 SQ SEQUENCE 106 AA; 11599 MW; FF0CCF5EEC2777A6 CRC64;

Query Match 5.9%; Score 7; DB 1; Length 106;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 ISSLLLL 11
 |||||
 DB 8 ISSLLLL 14
 |||||

RESULT 4

PRX2 RAT
 ID PRX2 RAT STANDARD; PRT; 107 AA.
 AC Q6R413;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)

```

28-FEB-2003 (Rel. 41, Last annotation update)
Prokineticin 2 precursor (PK2)
PROK2.
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
[1]
SEQUENCE FROM N.A.
STRAIN=Sprague-Dawley;
MEDLINE=22050031; PubMed=12054613;
Masuda Y., Takatsu Y., Terao Y., Kumano S., Ishibashi Y., Suenaga M.,
Abe M., Fukusumi S., Watanabe T., Shintani Y., Yamada T., Hinuma S.,
Inatomi N., Ohtaki T., Onda H., Fujino M.;
"Isolation and identification of EG-VEGF/prokineticins as cognate
ligands for two orphan G-protein-coupled receptors.";
Biochem. Biophys. Res. Commun. 293:395-402(2002).
[2]
EFFECT ON CIRCADIAN LOCOMOTOR ACTIVITY.
MEDLINE=22022134; PubMed=12024206;
Cheng M.Y., Bullock C.M., Li C., Lee A.G., Bermak J.C., Belluzzi J.,
Weaver D.R., Leslie F.M., Zhou Q.-Y.;
"Prokineticin 2 transmits the behavioural circadian rhythm of the
suprachiasmatic nucleus.";
Nature 417:405-410(2002).
-1- FUNCTION: May function as an output molecule from the
suprachiasmatic nucleus (SCN) that transmits behavioral circadian
rhythm. May also function locally within the SCN to synchronize
output. Potentially contracts gastrointestinal (GI) smooth muscle (By
similarity).
-1- SUBUNIT: Binds to PKR1 and PKR2, both are G-protein coupled
receptors.
-1- SUBCELLULAR LOCATION: Secreted (By similarity).
-1- TISSUE SPECIFICITY: Expressed at high levels in testis and at
lower levels in brain, lung, ovary, spleen, thymus and uterus.
-1- INDUCTION: Activated by Clock and Bmal1 heterodimers and light;
inhibited by period genes (PER1, PER2 and PER3) and cryptochrome
genes (CRY1 and CRY2) (Probable).
-1- SIMILARITY: BELONGS TO THE PROKINETICIN FAMILY.
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or send an email to license@isb-sib.ch).
-----
EMBL; AY089984; AA009105.1; -.
Signal peptide; Biological rhythms; Signal.
CHAIN 1 26
PROKINETICIN 2.
DISULFID 27 107
BY SIMILARITY.
DISULFID 33 45
BY SIMILARITY.
DISULFID 39 57
BY SIMILARITY.
DISULFID 44 85
BY SIMILARITY.
DISULFID 67 93
BY SIMILARITY.
DISULFID 87 103
BY SIMILARITY.
SEQUENCE 107 AA; 11594 MW; BDFP316DCB5PED0 CRC64;
very Match 5.9%; Score 7; DB 1; Length 107;
atches 7; Conservative 0; Pred.No.11; 0; Indels 0; Gaps 0;
8 LLLLLL 14
|||||
11 LLLLLL 17
JLT 5
} MOUSE
} PRK2 MOUSE STANDARD; PRT; 128 AA.
Q9QXU7; Q9QXU5; Q9QXU6;
16-OCT-2001 (Rel. 40, Created)
28-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Prokineticin 2 precursor (PK2) (Protein Bv8 homolog).
PROK2 OR Bv8.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
STRAIN=129/Sv;
MEDLINE=20047850; PubMed=10580115;
Wechselberger C., Puglisi R., Lepperdinger G., Boitani C., Kreil G.;
"The mammalian homologue of Bv8 from frog skin is mainly expressed in
spermatocytes.";
FEBS Lett. 462:177-181(1999).
[2]
SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
STRAIN=129/SvJ;
MEDLINE=20510004; PubMed=11054548;
Jilek A., Engel E., Beier D., Lepperdinger G.;
"Murine Bv8 gene maps near a syntenic breakpoint of mouse chromosome 6
and human 3p21.";
Gene 256:189-195(2000).
[3]
SEQUENCE FROM N.A. (ISOFORM 2), AND FUNCTION.
STRAIN=C57BL/6;
MEDLINE=2022134; PubMed=12024206;
Cheng M.Y., Bullock C.M., Li C., Lee A.G., Bermak J.C., Belluzzi J.,
Weaver D.R., Leslie F.M., Zhou Q.-Y.;
"Prokineticin 2 transmits the behavioural circadian rhythm of the
suprachiasmatic nucleus.";
Nature 417:405-410(2002).
[4]
SEQUENCE FROM N.A. (ISOFORM 1).
STRAIN=C57BL/6J; TISSUE=Testis;
MEDLINE=21085660; PubMed=11217851;
Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Arakawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,
Adzawa K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
Kuehl P., Lewis S., Matsuo Y., Nikola I., Pesole G., Quackenbush J.,
Schriml L.M., Stauble F., Suzuki R., Tomita M., Wagner L., Washio T.,
Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohseki S.,
Hayashizaki Y.;
"Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
-1- FUNCTION: May function as an output molecule from the
suprachiasmatic nucleus (SCN) that transmits behavioral circadian
rhythm. May also function locally within the SCN to synchronize
output. Potentially contracts gastrointestinal (GI) smooth muscle (By
similarity).
-1- SUBUNIT: Binds to PKR1 and PKR2, both are G-protein coupled
receptors.
-1- SUBCELLULAR LOCATION: Secreted.
-1- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=3;
Name=1; Synonyms=Bv8-a;
IsoId=Q9QXU7-1; Sequence=Displayed;
Name=2; Synonyms=Bv8-b;
IsoId=Q9QXU7-2; Sequence=VSP_005220;
Name=3;
IsoId=Q9QXU7-3; Sequence=VSP_005221;

```

```

-!- TISSUE SPECIFICITY: Expressed in the SCN and among a few other discrete brain areas, including the islands of Calleja, media 1 preoptic area of the hypothalamus and the shell of the nucleus accumbens. Highly expressed in testis. In the SCN, expression subjected to high amplitude of circadian oscillation.
-!- DEVELOPMENTAL STAGE: Expressed in mid-late pachytene spermatocytes at the stages VII, VIII and IX of the semiferous epithelial cycle.
-!- INDUCTION: Activated by Clock and Bmal heterodimers and light; inhibited by period genes (PER1, PER2 and PER3) and cryptochrome genes (CRY1 and CRY2).
-!- SIMILARITY: BELONGS TO THE PROKINECTIN FAMILY.

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EMBL; AF182064; AAF15259.1; -
EMBL; AF182065; AAF15260.1; -
EMBL; AF182066; AAF15261.1; -
EMBL; AF182067; AAG09439.1; -
EMBL; AF182068; AAG09439.1; JOINED.
EMBL; AF182069; AAG09439.1; -
EMBL; AF487280; AAM49572.1; -
EMBL; AK015462; BAB29857.1; -
HSSP; P25687; IIMT.
MGD; MGI:1354178; Prok2.
Neuropeptide; Biological rhythms; Signal; Alternative splicing.
POTENTIAL.
CHAIN 1 26
PROKINECTIN 2.
DISULFID 33 45
BY SIMILARITY.
DISULFID 39 57
BY SIMILARITY.
DISULFID 44 106
BY SIMILARITY.
DISULFID 67 114
BY SIMILARITY.
DISULFID 108 124
BY SIMILARITY.
VARSPPLIC 74 94
Missing (in isoform 2).
/FTID=VSP_005220.
SHVANGROERRAKRKKEVPWGRMRHETCPCLPGLAC
ISOFORM 3)
LRTSNFRIELARK -> VSVCTGILGVPSH (in isoform 3)
/FTID=VSP_005221.

SEQUENCE 128 AA; 14185 MW; 5F08BA17FDDB58C CRC64;

Query Match 5.9%; Score 7; DB 1; Length 128;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

8 LLLLLL 14
|||||
11 LLLLLL 17

ULT 6
RT MOUSE
CART_MOUSE STANDARD; PRT; 129 AA.
P56388; Q9QXZ8;
15-JUL-1998 (Rel. 36, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Cocaine- and amphetamine-regulated transcript protein precursor
[Contains: CART(1-52); CART(55-102)].
CART.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
STRAIN=129/SVJ;
MEDLINE=20080750; PubMed=10612705;
Adams L.D., Gong W., Vechia S.D., Hunter R.G., Kuhar M.J.;

```

```

RT "CART: from gene to function.";
RL Brain Res. 848:137-140(1999).
CC -!- FUNCTION: Satiety factor closely associated with the actions of
CC leptin and neuropeptide Y; this anorectic peptide inhibits both
CC normal and starvation-induced feeding and completely blocks the
CC feeding response induced by neuropeptide Y and regulated by leptin
CC in the hypothalamus (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted (Potential).
CC -!- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=2;
CC Names=Long;
CC IsoId=P56388-1; Sequences=Displayed;
CC Names=Short;
CC IsoId=P56388-2; Sequence=VSP_000793;
CC -!- SIMILARITY: BELONGS TO THE CART FAMILY.

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EMBL; AF148071; AAF24168.1; -
DR HSSP; Q16568; 1HY9.
DR MGD; MGI:1351330; Cart.
KW Neuropeptide; Neurotransmitter; Cleavage on pair of basic residues;
KW Alternative splicing; Signal.
FT SIGNAL 1 27
FT CHAIN 28 129
POTENTIAL.
COCAINE- AND AMPHETAMINE-REGULATED
TRANSCRIPT PROTEIN.
FT PEPTIDE 28 79
CART(1-52) (BY SIMILARITY).
FT PEPTIDE 82 129
CART(55-102) (BY SIMILARITY).
FT PEPTIDE 89 129
CART(62-102) (POTENTIAL).
FT DISULFID 95 113
BY SIMILARITY.
FT DISULFID 101 121
BY SIMILARITY.
FT DISULFID 115 128
BY SIMILARITY.
FT VARSPPLIC 54 66
Missing (in isoform Short).
/FTID=VSP_000793.
SEQUENCE 129 AA; 14285 MW; E4CA6CE70BEE6DF2 CRC64;

Query Match 5.9%; Score 7; DB 1; Length 129;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LLLLLL 14
|||||
DB 16 LLLLLL 22

RESULT 7
CART RAT
ID CART RAT STANDARD; PRT; 129 AA.
AC P49192;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cocaine- and amphetamine-regulated transcript protein precursor
DE [Contains: CART(1-52); CART(55-102)].
GN CART.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT).
RP STRAIN=Sprague-Dawley; TISSUE=Brain;
RX MEDLINE=95198122; PubMed=7891182;
RC Douglass J.O., McKinzie A.A., Couceyro P.;
RT "PCR differential display identifies a rat brain mRNA that is
RT transcriptionally regulated by cocaine and amphetamine.";
RT J. Neurosci. 15:2471-2481(1995).

```

[2] SEQUENCE OF 81-97, MASS SPECTROMETRY, AND DISULFIDE BONDS.
MEDLINE=98316718; PubMed=9654146;
Thim L., Nielsen P.F., Judge M.E., Andersen A.S., Diers I.,
Egel-Mitani M., Hastrup S.;
"Purification and characterisation of a new hypothalamic satiety
peptide, cocaine and amphetamine regulated transcript (CART),
produced in yeast.";
FEBS Lett. 428:263-268(1998).
-!- FUNCTION: Satiety factor closely associated with the actions of
leptin and neuropeptide Y; this anorectic peptide inhibits both
normal and starvation-induced feeding and completely blocks the
feeding response induced by neuropeptide Y and regulated by leptin
in the hypothalamus (By similarity).
-!- SUBCELLULAR LOCATION: Secreted (Potential).
-!- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
Name=Long;
IsoId=P49192-1; Sequence=Displayed;
Name=Short;
IsoId=P49192-2; Sequence=VSP 000794;
-!- TISSUE SPECIFICITY: Neuroendocrine tissues. Predominantly
expressed in the hypothalamus, pituitary, and longitudinal muscle-
myenteric plexus. Abundant expression is also seen in the
midbrain/thalamus and eye. A lower level expression is seen in the
other brain regions and adrenal.
-!- INDUCTION: By cocaine and amphetamine.
-!- SIMILARITY: BELONGS TO THE CART FAMILY.

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or send an email to license@isb-sib.ch).

EMBL; U10071; AAA87897.1; -;
HSP; Q16568; 1HY9.
Neuropeptide; Neurotransmitter; Cleavage on pair of basic residues;
Alternative splicing; Signal.
SIGNAL 1 27 POTENTIAL.
CHAIN 28 129 COCAINE- AND AMPHETAMINE-REGULATED
TRANSCRIPT PROTEIN.
PEPTIDE 28 79
PEPTIDE 82 129
PEPTIDE 89 129
DISULFID 95 113
DISULFID 101 121
DISULFID 115 128
VARSPIC 54 66
Missing (in isoform Short).
SEQUENCE 129 AA; 14140 MW; 0FDE283705BB2728 CRC64;
/Frid=VSP_000794.
Query Match 5.9%; Score 7; DB 1; Length 129;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

8 LLLLLL 14
| | | | |
16 LLLLLL 22

I.T. 8
TRYBB
R2A_TRYBB STANDARD; PRT; 145 AA.
O15883;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
60S ribosomal protein L27a (L29).
REL27A.
Trypanosoma brucei.

OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxID=5702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Treu 667;
RA Brown S.V., Williams N.;
RT "The 60S ribosomal protein L27a (L29) gene of Trypanosoma brucei.";
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE L15P FAMILY OF RIBOSOMAL PROTEINS.

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or send an email to license@isb-sib.ch).

CC EMBL; U96757; AAB62182.1; -;
DR InterPro; IPR001196; Ribosomal_L15.
DR Pfam; PF00256; L15; 1.
DR PROSITE; PS00475; RIBOSOMAL_L15; FALSE_NEG.
KW Ribosomal protein.
SQ SEQUENCE 145 AA; 16294 MW; DAC63E602D706D7C CRC64;
Query Match 5.9%; Score 7; DB 1; Length 145;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 85 KKTRHOR 91
DB 6 KKTRHOR 12

RESULT 9
RNS6_BOVIN STANDARD; PRT; 154 AA.
ID RNS6_BOVIN
AC P08904; Q95324; Q9TUP9;
DT 01-NOV-1988 (Rel. 09, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ribonuclease K6 precursor (EC 3.1.27.-) (RNase K6) (K5b) (RNase K2).
GN RNASE6 OR RNS6 OR RK6B.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC Tissue=Spinal cord;
RA Pietrowski D., Foerster M.;
RT "Complete cDNA sequence of a bovine ribonuclease k6b (brk6b).";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 28-154.
RX MEDLINE=89034023; PubMed=3182769;
RA Irie M., Nitta R., Ohgi K., Niwata Y., Watanabe H., Iwama M.,
RA Beintema J.J., Senda A., Takizawa Y.;
RT "Primary structure of a non-secretory ribonuclease from bovine
kidney.";
RL J. Biochem. 104:289-296(1988).
RN [3]
RP SEQUENCE OF 28-154.
RC Tissue=Kidney;
RX MEDLINE=85261183; PubMed=3926759;
RA Niwata Y., Ohgi K., Senda A., Takizawa Y., Irie M.;
RT "Purification and properties of bovine kidney ribonucleases.";
RL J. Biochem. 97:923-934(1985).
RN [4]
RP SEQUENCE OF 37-129 FROM N.A.
RX MEDLINE=96433147; PubMed=8836175;
RA Rosenberg H.F., Dyer K.D.;

"Molecular cloning and characterization of a novel human ribonuclease (Rnase k6): increasing diversity in the enlarging ribonuclease gene family." ;

Nucleic Acids Res. 24:3507-3513 (1996).

-1- FUNCTION: PYRIMIDINE SPECIFIC NUCLEASE WITH A PREFERENCE FOR U.
-1- SUBCELLULAR LOCATION: LYCOSOMAL (PROBABLE); MATRIX OF EOSINOPHIL'S
-1- LARGE SPECIFIC GRANULE.

-1- TISSUE SPECIFICITY: Kidney.

-1- SIMILARITY: Belongs to the pancreatic ribonuclease family.

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EMBL; AF184025; AAD44349.1; -;
EMBL; U64997; AAC48633.1; -;
PIR; S72363; S72363.

HSRP; P00656; 2RNS.

InterPro; IPR001427; RNaseA.

Pfam; PF00074; rnaseA; 1.

PRINTS; PR00794; RIBONUCLEASE.

ProDom; PD000535; RNaseA; 1.

SMART; SM00092; RNaseA; 1.

PROSITE; PS00127; RNaseA; 1.

Hydrolase; Nuclease; Endonuclease; Glycoprotein; Signal.

SIGNAL

CHAIN 28 154 RIBONUCLEASE K6.

ACT_SITE 42 42 BY SIMILARITY.

ACT_SITE 65 65 BY SIMILARITY.

ACT_SITE 149 149 BY SIMILARITY.

DISULFID 50 108 BY SIMILARITY.

DISULFID 64 118 BY SIMILARITY.

DISULFID 82 133 BY SIMILARITY.

DISULFID 89 96 BY SIMILARITY.

CARBOHYD 59 59 N-LINKED (GLCNAC. .) (POTENTIAL).

CARBOHYD 104 104 N-LINKED (GLCNAC. .) (POTENTIAL).

CONFLICT 45 51 PRLQCN -> SRIIPS (IN REF. 3).

CONFLICT 65 65 K -> N (IN REF. 4).

CONFLICT 153 154 VV -> YF (IN REF. 2 AND 3).

SEQUENCE 154 AA; 17660 MW; 9325DF841EF39C11 CRC64;

Query Match 5.9%; Score 7; DB 1; Length 154;
est Local Similarity 100.0%; Pred. No. 16;
atches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

6 SLLLLLL 12

|||||

9 SLLLLLL 15

ULT 10

M_SV40

TASM SV40 STANDARD; PRT; 174 AA.

P03081;

21-JUL-1986 (Rel. 01, Created)

21-JUL-1986 (Rel. 01, Last sequence update)

28-FEB-2003 (Rel. 41, Last annotation update)

Small T antigen. (SV40).

Simian virus 40 (SV40).

Viruses; GEDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.

NCBI_TaxID=10633;

[1]

SEQUENCE FROM N.A.

MEDLINE=78159686; PubMed=205947;

Reddy V.B., Thimmapaya B., Dhar R., Subramanian K.N., Zain B.S.,

Pan J., Ghosh P.K., Celma M.L., Weisman S.M.;

"The genome of simian virus 40.";

Science 200:494-502(1978).

[2]

RP SEQUENCE FROM N.A.

RC STRAIN=776;

RX MEDLINE=78156432; PubMed=205802;

RA Fiers W., Contreras R., Haegeman G., Rogiers R., van de Voorde A.,

van Heuverswyn H., van Herreweghe J., Volckaert G., Ysebaert M.;

RT "Complete nucleotide sequence of SV40 DNA.";

RL Nature 273:113-120(1978).

RN [3]

RP INHIBITION OF PHOSPHATASE PP2A ACTIVITY.

RX MEDLINE=91172186; PubMed=1848668;

RA Scheidtmann K.H., Mumby M.C., Rundell K., Walter G.;

RT "Dephosphorylation of simian virus 40 large-T antigen and p53 protein

by protein phosphatase 2A: inhibition by small-t antigen.";

RL Mol. Cell. Biol. 11:1996-2003(1991).

RN [4]

RP BINDING IN VITRO TO PP2A.

RX MEDLINE=91172185; PubMed=1706474;

RA Yang S.-L., Lickteig R.L., Estes R., Rundell K., Walter G.;

RT "Control of protein phosphatase 2A by simian virus 40 small-t

antigen.";

RL Mol. Cell. Biol. 11:1988-1995(1991).

CC -1- SUBUNIT: BINDS IN VITRO TO PP2A AND INTERACTS WITH THE A SUBUNIT

AND THIS INTERACTION INHIBITS ENZYME ACTIVITY.

CC -1- MISCELLANEOUS: THE INITIAL 82 RESIDUES OF THE LARGE T AND SMALL T

ANTIGENS FROM SV40 ARE CODED BY THE SAME NUCLEOTIDE SEQUENCE.

CC -1- SIMILARITY: Contains 1 J domain.

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CC EMBL; J02400; AAB59925.1; -;

PIR; C03631; TVVPA4.

InterPro; IPR001623; DnaJ N.

InterPro; IPR003354; Papo_T_antigen.

Pfam; PF00236; DnaJ; 1.

Pfam; PF02380; Papo_T_antigen; 1.

SMART; SM00271; DnaJ; 1.

PROSITE; PS00636; DnaJ_1; FALSE NEG.

PROSITE; PS50076; DnaJ_2; 1.

Early protein; Acetylation.

DOMAIN 12 75 J-DOMAIN.

MOD_RES 1 1 ACETYLATION.

SEQUENCE 174 AA; 20449 MW; 91EC925ED2E29668 CRC64;

Query Match 5.9%; Score 7; DB 1; Length 174;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 SSLNPGV 28

|||||

Db 86 SSLNPGV 92

RESULT 11

YP37 DEIRA

ID_YP37 DEIRA STANDARD; PRT; 202 AA.

AC Q98RF5;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Hypothetical protein PR2537.

GN DR2537.

OS Deinococcus radiodurans.

OC Bacteria; Deinococcus-Thermus; Deinococci; Deinococcales;

OC Deinococcaceae; Deinococcus.

OX NCBI_TaxID=1299;

RN [1]

"Whole-genome random sequencing and assembly of Haemophilus influenzae
 Rd.";
 RL Science 269:496-512(1995).
 CC -!- SIMILARITY: STRONG, TO E.COLI YGIM.

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 CC or send an email to license@isb-sib.ch).

 CC EMBL: U32834; AAC23249.1; -;
 CC PIR: C64038; C64038.
 CC TIGR: H11605; -;
 CC InterPro: IPR003646; SH3_bac.
 CC SMART: SM00297; SH3b; 1_bac.
 CC Hypothetical protein; Transmembrane; Signal; Complete proteome.
 CC SIGNAL 1 23 POTENTIAL.
 CC CHAIN 24 203 HYPOTHETICAL PROTEIN H11605.
 CC TRANSMEM 167 189 POTENTIAL.
 CC SEQUENCE 203 AA; 23112 MW; FAFCE229FD29C05 CRC64;

 CC Query Match 5.9%; Score 7; DB 1; Length 203;
 CC Best Local Similarity 100.0%; Pred.No.20;
 CC Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 CC QY 4 LISSLL 10
 CC DB 8 LISSLL 14

 CC RESULT 13
 CC YK07_YEAST
 CC ID YK07_YEAST STANDARD; PRT; 205 AA.
 CC IC P36061;
 CC DT 01-JUN-1994 (Rel. 29, Last sequence update)
 CC DT 01-JUN-1994 (Rel. 29, Last sequence update)
 CC DT 01-OCT-1994 (Rel. 30, Last annotation update)
 CC DE Hypothetical 22.7 kDa protein in SDH1-CIM5/YTA3 intergenic region.
 CC GN YKJ147C OR YKJ1601.
 CC OS Saccharomyces cerevisiae (Baker's yeast).
 CC OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 CC OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 CC OX NCBI_TaxID=4932;
 CC RN [1]
 CC RP SEQUENCE FROM N.A.
 CC RC STRAIN=S288C;
 CC RX MEDLINE=94378720; PubMed=8091859;
 CC RA Vandenbol M., Bolle P.-A., Dion C., Portetelle D., Hilger F.;
 CC RT "DNA sequencing of a 36.2 kb fragment located between the FAS1 and
 CC RT LAP loci of chromosome XI of Saccharomyces cerevisiae.";
 CC RL Yeast 10:S35-S40(1994).

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 CC EMBL: Z26877; CAA81507.1; -;
 CC PIR: Z28146; CAA81987.1; -;
 CC TIGR: S37804; S37804.
 CC SGD: S0001630; YKJ147C.
 CC Hypothetical protein.
 CC SEQUENCE 205 AA; 22673 MW; 01F1625B361D9DCE CRC64;

 CC Query Match 5.9%; Score 7; DB 1; Length 205;
 CC Best Local Similarity 100.0%; Pred.No.20;
 CC Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

8 LLLLLL 14
|||||
78 LLLLLL 84

ULT 14
2 MOUSE
  EF2801;          STANDARD;      PRT;    209 AA.
01-OCT-1996 (Rel. 34, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
Ephrin-A2 precursor (EPH-related receptor tyrosine kinase ligand 6)
(ELF-6) (ELF-1) (CEK7-ligand) (CEK7-L).
EFNA2 OR EPLG6 OR LERK6 OR ELF1 OR EPL6.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A.
STRAIN=Swiss Webster; TISSUE=Brain;
MEDLINE=95007776; PubMed=7522971;
Cheng H.J., Flanagan J.G.;
"Identification and cloning of ELF-1, a developmentally expressed
ligand for the Mek4 and Erk receptor tyrosine kinases.";
Cell 79:157-168(1994).
[2]
SEQUENCE FROM N.A.
TISSUE=Brain;
MEDLINE=95181289; PubMed=7876076;
Shao H., Lou L., Pandey A., Verderame M.P., Siever D.A., Dixit V.M.;
"cDNA cloning and characterization of a Cdk7 receptor
protein-tyrosine kinase ligand that is identical to the ligand
(ELF-1) for the Mek4 and Erk receptor protein-tyrosine kinases.";
J. Biol. Chem. 270:3467-3470(1995).
-1- SUBUNIT: BINDS TO THE RECEPTOR TYROSINE KINASES EPHA3, EPHA4 AND
EPHA5.
-1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
(Potential).
-1- SIMILARITY: BELONGS TO THE EPHRIN FAMILY.
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EMBL; U14941; AAA53636.1; -.
EMBL; U14752; AAA68520.1; -.
PIR; A54984; A54984.
MGD; MGI:102707; EFna2.
InterPro; IPR001799; Ephrin.
Pfam; PF00812; Ephrin; 1.
PRINTS; PR01347; EPHRIN.
ProDom; PD002533; Ephrin; 1.
PROSITE; PS01299; EPHRIN; 1.
Glycoprotein; GPI-anchor; Signal.
CHAIN 1 20 POTENTIAL.
EPHRIN-A2.
CARBOHYD 38 38 N-LINKED (GLCNAC. .) (POTENTIAL).
CARBOHYD 170 170 N-LINKED (GLCNAC. .) (POTENTIAL).
CARBOHYD 184 184 N-LINKED (GLCNAC. .) (POTENTIAL).
SEQUENCE 209 AA; 23586 MW; F1997545F25B9ABC CRC64;
Query Match 5.9%; Score 7; DB 1; Length 209;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
8 LLLLLL 14

Db 12 LLLLLL 18
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RESULT 15
CLDD MOUSE
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AC Q920S4;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Claudin-13.
GN CLDN13.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
OX [1]
SEQUENCE FROM N.A.
RP Morita K., Furuse M., Tsukita S.;
RA Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
RL [2]
SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Embryonic liver;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldi M.F.,
RA Brownstein M.J., Bult C., Flechner C., Fujita M., Gariboldi M.,
RA Guscinich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nardone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Synhak-Boris A., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wyszewski A., Yoshida K., Hasegawa Y., Kawaji H., Kohteki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
CC -1- FUNCTION: COMPONENT OF TIGHT JUNCTION (TJ) STRANDS.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to the claudin family.
-----
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or send an email to license@isb-sib.ch).
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EMBL; AF124428; AAD17322.1; -.
DR EMBL; AK010869; BAB27234.1; -.
DR MGD; MGI:1913102; Cldn13.
InterPro; IPR006188; Claudin sup.
DR InterPro; IPR004031; PMP22 Claudin.
DR Pfam; PF00822; PMP22 Claudin; 1.
DR PROSITE; PS01346; CLAUDIN; 1.
Tight junction; Transmembrane
TRANSMEM 9 29 POTENTIAL.
FT TRANSMEM 81 101 POTENTIAL.
FT TRANSMEM 119 139 POTENTIAL.
FT TRANSMEM 166 186 POTENTIAL.
SQ SEQUENCE 211 AA; 23503 MW; 53CC8697C53D46BE CRC64;
Query Match 5.9%; Score 7; DB 1; Length 211;
Best Local Similarity 100.0%; Pred. No. 20;

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ches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

6 SLLLLL 12

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169 SLLLLL 175

h completed: February 18, 2004, 15:44:22
ime : 32 secs

GenCore version 5.1.6
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otein - protein search, using sw model

n: February 18, 2004, 15:31:05 ; Search time 34 Seconds
(without alignments)
903.184 Million cell updates/sec

ct score: 119
nce: 1 MKVLISLLLLPLMLMSV.....SRACQFLKQCLRSFALPL 119

ng table: OLIGO
Gapop 60.0 , Gapext 60.0

hed: 830525 seqs, 258052604 residues

size : 0
l number of hits satisfying chosen parameters: 830525

num DB seq length: 0
num DB seq length: 2000000000

rocessing: Listing first 45 summaries

- ase :
- 1: SP TREMBL 23:*
 - 2: sp archa:
 - 3: sp bacteria:
 - 4: sp fungi:
 - 5: sp invertebrate:
 - 6: sp mammal:
 - 7: sp mhc:
 - 8: sp organelle:
 - 9: sp page:
 - 10: sp plant:
 - 11: sp rodent:
 - 12: sp virus:
 - 13: sp vertebrate:
 - 14: sp unclassified:
 - 15: sp rvirus:
 - 16: sp bacteriap:
 - 17: sp archaep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

lt	Score	Query Match	Length	DB	ID	Description
1	13	10.9	128	11	Q8R3U6	Q8R3U6 mus musculus
2	9	7.6	309	16	Q8EV11	Q8EV11 mycoplasma
3	9	7.6	842	11	Q8R432	Q8R432 mus musculus
4	9	7.6	842	11	Q8DRH3	Q8DRH3 mus musculus
5	9	7.6	842	11	Q8VCU2	Q8VCU2 mus musculus
6	8	6.7	86	16	Q84166	Q84166 Chlamydia t
7	8	6.7	109	16	P71060	P71060 bacillus su
8	8	6.7	181	10	Q9FJN3	Q9FJN3 arabidopsis
9	8	6.7	182	10	Q8L6Z5	Q8L6Z5 arabidopsis
10	8	6.7	277	2	O69120	O69120 burkholderi
11	8	6.7	277	2	Q9AEV4	Q9AEV4 burkholderi
12	8	6.7	285	2	O33629	O33629 eaccharopol
13	8	6.7	332	8	Q8HEH7	Q8HEH7 chiroxiphia
14	8	6.7	360	11	Q8C252	Q8C252 mus musculus
15	8	6.7	363	11	Q8K295	Q8K295 mus musculus
16	8	6.7	384	16	Q8ESE3	Q8ESE3 oceanobacil

17	8	6.7	408	16	Q92QTS	Q92QTS rhizobium m
18	8	6.7	449	16	Q9ABE3	Q9ABE3 caulobacter
19	8	6.7	453	2	Q93SO0	Q93SO0 pseudomonas
20	8	6.7	453	2	Q93SP9	Q93SP9 pseudomonas
21	8	6.7	453	2	Q93SQ2	Q93SQ2 pseudomonas
22	8	6.7	453	2	Q933J5	Q933J5 pseudomonas
23	8	6.7	453	2	Q93451	Q93451 pseudomonas
24	8	6.7	453	2	Q93SQ3	Q93SQ3 pseudomonas
25	8	6.7	453	2	Q93SQ1	Q93SQ1 pseudomonas
26	8	6.7	453	16	Q51449	Q51449 pseudomonas
27	8	6.7	494	17	Q8U246	Q8U246 pyrococcus
28	8	6.7	594	16	Q8BXP5	Q8BXP5 mycoplasma
29	8	6.7	613	8	Q8HM93	Q8HM93 bregmaceros
30	8	6.7	827	16	Q8CPL9	Q8CPL9 scapyllococ
31	8	6.7	896	5	Q94891	Q94891 drosophila
32	8	6.7	1015	4	Q9Y6L7	Q9Y6L7 homo sapien
33	8	6.7	1236	3	Q9C105	Q9C105 schizosacch
34	8	6.7	1305	16	Q8ZB96	Q8ZB96 versinia pe
35	7	5.9	41	8	Q8HE48	Q8HE48 thraxan acu
36	7	5.9	41	8	Q8HE47	Q8HE47 thraxan ebe
37	7	5.9	52	16	Q8ZDY9	Q8ZDY9 yersinia pe
38	7	5.9	68	10	Q8RYJ4	Q8RYJ4 oryza sativ
39	7	5.9	76	13	Q8J66	Q8J66 oncothynchu
40	7	5.9	89	10	Q8S6T9	Q8S6T9 oryza sativ
41	7	5.9	89	11	Q9WUG8	Q9WUG8 mus musculu
42	7	5.9	90	4	Q9UCV8	Q9UCV8 homo sapien
43	7	5.9	90	17	Q8U0W3	Q8U0W3 pyrococcus
44	7	5.9	92	10	Q9AS65	Q9AS65 oryza sativ
45	7	5.9	94	11	Q8K3Z3	Q8K3Z3 rattus norv

ALIGNMENTS

RESULT 1

Q8R3U6 PRELIMINARY; PRT; 128 AA.
ID Q8R3U6;
AC Q8R3U6;
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Similar to hypothetical gene LOC125944.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC024561; AAH24561.1; -;
SQ SEQUENCE 128 AA; 14043 MW; CCE67DA04D23D7DF CRC64;

Query Match 10.9%; Score 13; DB 11; Length 128;
Best Local Similarity 100.0%; Pred. No. 2.4e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 45 EGGQECCKDWFL 57
DB 45 EGGQECCKDWFL 57

RESULT 2

Q8EV11 PRELIMINARY; PRT; 309 AA.
ID Q8EV11;
AC Q8EV11;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Conserved hypothetical protein.
GN MPE7560.
OS Mycoplasma penetrans.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.

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NCBI_TaxID=28227;
[1]
SEQUENCE FROM N.A.
STRAIN=HF-2;
MEDLINE=22354719; PubMed=12466555;
Sasaki Y., Ishikawa J., Yamashita A., Oshima K., Kenri T., Furuya K.,
Yoshino C., Horino A., Shiba T., Sasaki T., Hattori M.;
"The complete genomic sequence of Mycoplasma penetrans, an
intracellular bacterial pathogen in humans.";
Nucleic Acids Res. 30:5293-5300(2002).
EMBL; AF004173; BAC4550.1; -.
Hypothetical protein; Complete proteome.
SEQUENCE 309 AA; 36285 MW; 045179015A472DD9 CRC64;

Query Match 7.6%; Score 9; DB 16; Length 309;
Best Local Similarity 100.0%; Pred. No. 0.65;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

4 LISSLLLLL 12
|||||
171 LISSLLLLL 179

JLT 3
132 Q8R432 PRELIMINARY; PRT; 842 AA.
Q8R432;
01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Glycosylphosphatidylinositol phospholipase D.
GPLD1.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A.
TISSUE=Liver;
Lund T., Flores-Borja F.;
"Characterization of the mouse glycosylphosphatidylinositol
phospholipase D (GPLD gene).";
Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
EMBL; AY081194; AAL87452.1; -.
MGD; MGI:106604; Gpld1.
InterPro; IPR000413; Integrin_alpha.
Pfam; PF01839; FG-GAP; 6.
SMART; SM00191; Int_alpha; 5.
SEQUENCE 842 AA; 93653 MW; 2458B409EB515CD2 CRC64;

Query Match 7.6%; Score 9; DB 11; Length 842;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

JLT 4
843 Q9DBH3 PRELIMINARY; PRT; 842 AA.
Q9DBH3;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2003 (TrEMBLrel. 20, Last annotation update)
Glycosylphosphatidylinositol specific phospholipase D1.
GPLD1.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A.
TISSUE=Liver;
Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
Kadoya K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
Schriml L.M., Staubli F., Suzuki R., Tonita M., Wagner L., Washio T.,
Sakai K., Okido I., Furuno M., Aono H., Baidarelli R., Barsh G.,
Blake J., Boicelli D., Bojunga N., Carninci P., de Bonaudo M.F.,
Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
Gustincich S., Hill D., Hofmann M., Hume D.A., Kaniya M., Lee N.H.,
Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
Nordone P., Ring K., Ringwald M., Rodriguez I., Sakamoto N.,
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohzuki S.,
Hayaishizaki Y.;
"Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
EMBL; AK004957; BAB23698.1; -.
MGD; MGI:106604; Gpld1.
InterPro; IPR001028; Gprt_Plipased.
DR Pfam; PF01839; FG-GAP; 6.
DR PRINTS; PR00718; PHPLIPASED.
DR SMART; SM00191; Int_alpha; 5.
SQ SEQUENCE 842 AA; 93646 MW; 119B25C835545533 CRC64;

Query Match 7.6%; Score 9; DB 11; Length 842;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 SSSLLLLLPL 14
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Db 8 SSSLLLLLPL 16

RESULT 5
Q8VCU2 PRELIMINARY; PRT; 842 AA.
ID Q8VCU2
AC Q8VCU2;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Glycosylphosphatidylinositol specific phospholipase D1.
GN GPLD1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CX Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A.
TISSUE=Liver;
Strausberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC019146; AAR19146.1; -.
MGD; MGI:106604; Gpld1.
InterPro; IPR001028; Gprt_Plipased.
DR Pfam; PF01839; FG-GAP; 4.
DR PRINTS; PR00718; PHPLIPASED.
DR SMART; SM00191; Int_alpha; 5.
SQ SEQUENCE 842 AA; 93623 MW; 2458B409EB550DD2 CRC64;

Query Match 7.6%; Score 9; DB 11; Length 842;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 SSSLLLLLPL 14
|||||
Db 8 SSSLLLLLPL 16

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8 SSLLLLLPL 16

LT 6
56
O84166 PRELIMINARY; PRT; 86 AA.
O84166;
01-NOV-1998 (TREMELrel. 08, Created)
01-NOV-1998 (TREMELrel. 08, Last sequence update)
01-MAR-2002 (TREMELrel. 20, Last annotation update)
Hypothetical protein CT164.
CT164.
Chlamydia trachomatis.
Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
NCBI_TaxID=813;
[1]
SEQUENCE FROM N.A.
STRAIN=D/UN-3/Cx;
MEDLINE=99000809; PubMed=9784136;
Stephens R.S., Kalman S., Lamm C.J., Fan J., Marathe R., Aravind L.,
Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
Davis R.W.;
"Genome sequence of an obligate intracellular pathogen of humans:
Chlamydia trachomatis."
Science 282:754-759(1998).
EMBL; AB001290; AAC67755.1; -.
Hypothetical protein; Complete proteome.
SEQUENCE 86 AA; 9162 MW; 55ED2981A0237F9B CRC64;
ery Match 6.7%; Score 8; DB 16; Length 86;
st Local Similarity 100.0%; Pred. No. 2.4;
atches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
5 ISSLLLLL 12
46 ISSLLLLL 53

LT 7
60
P71060 PRELIMINARY; PRT; 109 AA.
P71060; O08179;
01-FEB-1997 (TREMELrel. 02, Created)
01-FEB-1997 (TREMELrel. 02, Last sequence update)
01-MAR-2002 (TREMELrel. 20, Last annotation update)
Hypothetical protein yvfa.
yfa.
Bacillus subtilis.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=1423;
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SEQUENCE FROM N.A.
STRAIN=168TRP;
Fabret C., Quentin Y., Chapal N., Guiseppe A., Haiech J., Denizot F.;
Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.
[2]
SEQUENCE FROM N.A.
Denizot F.C.;
Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
[3]
SEQUENCE FROM N.A.
STRAIN=168;
MEDLINE=98044033; PubMed=9384377;
Kunst F., Ogasawara N., Moser I., Albertini A.M., Alloni G.,
Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
Bourissier R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
Fritz C., Fujita M., Fujita Y., Funa S., Gallizzi A., Galleron N.,
Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,

RA Guiseppe G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Mael C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Presecan E., Pujic P., Putelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sekiguchi J., Sekowska A., Seror S.J., Seror P., Shin B.S., Soldo B.,
RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Takakoshi A., Tanaka T., Terpetra P., Tognoni A.,
RA Tosato V., Uchiyama S., Vanderbol M., Vannier F., Vassarotti A.,
RA Viari A., Wambutt R., Wedler E., Wedler K., Weitzenecker T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.,
RT "The complete genome sequence of the gram-positive bacterium Bacillus
RT subtilis.";
RL Nature 390:249-256(1997).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RA Kunst F., Ogasawara N., Yoshikawa H., Danchin A.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z71928; CAA96478.1; -.
DR EMBL; Z94043; CAB07994.1; -.
DR EMBL; Z99121; CAB15432.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 109 AA; 12046 MW; F0C5F36DE3BD3D68 CRC64;
Query Match 6.7%; Score 8; DB 16; Length 109;
Best Local Similarity 100.0%; Pred. No. 2.9; 0; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 0;
QY 7 SLLLLLPL 14
DB 92 SLLLLLPL 99

RESULT 8
Q9FJM3 PRELIMINARY; PRT; 181 AA.
AC Q9FJM3;
DT 01-MAR-2001 (TREMELrel. 16, Created)
DT 01-MAR-2001 (TREMELrel. 16, Last sequence update)
DT 01-JUN-2002 (TREMELrel. 21, Last annotation update)
DE Phytoeyanin/early nodulin-like protein.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Columbia;
RX MEDLINE=98403884; PubMed=9734815;
RA Kotani H., Nakamura Y., Sato S., Asamizu E., Kaneko T., Miyajima N.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. VI.
RT Sequence features of the regions of 1,367,185 bp covered by 19
RT physically assigned pl and TAC clones.";
RL DNA Res. 5:203-216(1998).
DR EMBL; AB013396; BAB08862.1; -.
DR HSSP; P00303; 2CBP.
DR InterPro; IPR003245; P1cyanin like.
DR Pfam; PF02298; Cu_bind_like.1.
DR ProDom; PD003122; P1cyanin like.1.
SQ SEQUENCE 181 AA; 20216 MW; DCE3EE93CAED921 CRC64;
Query Match 6.7%; Score 8; DB 10; Length 181;

st Local Similarity 100.0%; Pred. No. 4.5;
atches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
7 SLLLLPL 14
170 SLLLLPL 177

ULT 9
Z5 Q8L6Z5 PRELIMINARY; PRT; 182 AA.
Q8L6Z5; 01-OCT-2002 (TREMBlrel. 22, Created)
01-OCT-2002 (TREMBlrel. 22, Last sequence update)
01-MAR-2003 (TREMBlrel. 23, Last annotation update)
Phytoeyanin/early nodulin-like protein.
AT5G5920.
Arabidopsis thaliana (Mouse-ear cross).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsids.
NCBI_TaxID=3702;
[1]
SEQUENCE FROM N.A.
Tripp M., Southwick A., Karlin-Neumann G., Nguyen M., Miranda M.,
Palm C.J., Bowser L., Jones T., Banh J., Carrinci P., Chen H.,
Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,
Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,
Ecker J., Theologis A., Davis R.W.;
Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
EMBL; AY140062; AAM98203.1; -
InterPro; IPR003245; Plicyanin-like.
Pfam; PF02298; Cu_bind-like; 1.
ProDom; PD003122; Plicyanin-like; 1.
SEQUENCE 182 AA; 20343 MW; AA120684C34207CB CRC64;

Query Match 6.7%; Score 8; DB 10; Length 182;
est Local Similarity 100.0%; Pred. No. 4.5;
atches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

7 SLLLLPL 14
171 SLLLLPL 178

ULT 10
120 C69120 PRELIMINARY; PRT; 277 AA.
O69120; 01-AUG-1998 (TREMBlrel. 07, Created)
01-AUG-1998 (TREMBlrel. 07, Last sequence update)
01-MAR-2003 (TREMBlrel. 23, Last annotation update)
Putative ABC-2 transporter integral membrane component.
WZM
Burkholderia pseudomallei (Pseudomonas pseudomallei).
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Burkholderiaceae; Burkholderia.
NCBI_TaxID=28450;
[1]
SEQUENCE FROM N.A.
STRAIN=1026b;
MEDLINE=99441012; PubMed=9988493;
DeShazer D., Brett P.J., Woods D.E.;
"The type II O-antigenic polysaccharide moiety of Burkholderia
pseudomallei lipopolysaccharide is required for serum resistance and
virulence."
Mol. Microbiol. 30:1081-1100(1998).
EMBL; AF064070; AAD05458.1; -
InterPro; IPR000412; ABC_transp2.
Pfam; PF01061; ABC2_membrane; 1.
PRINTS; PR00164; ABC2TRNSPORT.
SEQUENCE 277 AA; 30644 MW; 01E50FEE7378BF7 CRC64;

Query Match 6.7%; Score 8; DB 2; Length 277;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 LLPLMLMS 18
Db 165 LLPLMLMS 172

RESULT 11
Q9AEV4 PRELIMINARY; PRT; 277 AA.
ID Q9AEV4
AC Q9AEV4; 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Putative ABC-2 transporter integral membrane component.
GN WZM.
OS Burkholderia mallei (Pseudomonas mallei).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Burkholderia.
ON NCBI_TaxID=13373;
RN [1]
RP SEQUENCE FROM N.A.
RA Burtinck M.N., Brett P.J., Woods D.E.;
"Physical and Molecular Characterization of Lipopolysaccharide O-
antigens from Burkholderia mallei";
Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL; AY028370; AAK27395.1; -
DR InterPro; IPR000412; ABC_transp2.
DR Pfam; PF01061; ABC2_membrane; 1.
DR PRINTS; PR00164; ABC2TRNSPORT.
SQ SEQUENCE 277 AA; 30628 MW; ASA50FEE7379636 CRC64;

Query Match 6.7%; Score 8; DB 2; Length 277;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 LLPLMLMS 18
Db 165 LLPLMLMS 172

RESULT 12
O33629 PRELIMINARY; PRT; 285 AA.
ID O33629
AC O33629;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE ORF homologous to Escherichia coli and Salmonella typhimurium dnaE
gene (Fragment).
OS Saccharopolyspora erythraea (Streptomyces erythraeus).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Pseudonocardineae; Pseudonocardaceae; Saccharopolyspora.
ON NCBI_TaxID=1836;
RN [1]_TaxID=1836;
RP SEQUENCE FROM N.A.
RX MEDLINE=92121109; PubMed=1732208;
RA Andersen J.F., Hutchinson C.R.;
RT "Characterization of Saccharopolyspora erythraea cytochrome P-450
genes and enzymes, including 6-deoxyerythronolide B hydroxylase";
RL J. Bacteriol. 174:725-735(1992).
DR EMBL; M83110; AAA26482.1; -
FT NON-TER
SQ SEQUENCE 285 AA; 30109 MW; EA741E79E4782B36 CRC64;

Query Match 6.7%; Score 8; DB 2; Length 285;
Best Local Similarity 100.0%; Pred. No. 6.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 ARGHDRG 36

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147 ARGHRRG 154

LT 13
E7
Q8H77 PRELIMINARY; PRT; 332 AA.
01-MAR-2003 (T-EMBLrel. 23, Created)
01-MAR-2003 (T-EMBLrel. 23, Last sequence update)
01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
Cytochrome b (Fragment).
CYTB.
Chiroxiphia caudata.
Mitochondrion.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Passeriformes; Pipridae; Chiroxiphia.
NCBI_TaxID=196027;
[1]
SEQUENCE FROM N.A.
Johansson U.S., Irestedt M., Parsons T.J., Ericson P.G.P.;
"Basal phylogenetic relationships within Tyrannidae";
Auk 0:0-0(2002). AN76175.1; -.
EMBL; AF453819; AN76175.1; -.
Mitochondrion.
NON TER 1
SEQUENCE 332 AA; 37577 MW; C037BC61B1CC00A2 CRC64;
Query Match 6.7%; Score 8; DB 8; Length 332;
Best Local Similarity 100.0%; Pred. No. 7.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

8 LLLLLPLM 15
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186 LLLLLPLM 193

ILT 14
:52
Q8C252 PRELIMINARY; PRT; 360 AA.
Q8C252;
01-MAR-2003 (T-EMBLrel. 23, Created)
01-MAR-2003 (T-EMBLrel. 23, Last sequence update)
01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
Low density lipoprotein receptor-related protein associated protein
1.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A.
STRAIN=NOD;
MEDLINE=22354683; PubMed=12466851;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
EMBL; AK089250; BAC40814.1; -.
SEQUENCE 360 AA; 42157 MW; DF3D442BD9C18F80 CRC64;
Query Match 6.7%; Score 8; DB 11; Length 360;
Best Local Similarity 100.0%; Pred. No. 7.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

9 LLLLLPLM 16
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19 LLLLLPLM 26

JLT 15
295

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